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OM nucleic - nucleic search, using sw model

Run on:         July 26, 2006, 15:59:07 ; Search time 622.366 Seconds
                                          (without alignments)
                                          375.125 Million cell updates/sec

Title:          US-10-743-384-2
Perfect score:  19
Sequence:       1 tgcgggacttaacccaaca 19

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:      24217294

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Database :       Published_Applications_NA_Main:*
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                2:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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                11:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                12:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                13:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
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                16:  /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                    SUMMARIES

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Result              Query
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	3	19	100.0	19	9	US-10-743-384-2	Sequence 2, Appli
c	4	19	100.0	19	9	US-10-743-384-8	Sequence 8, Appli
	5	19	100.0	20	6	US-10-233-223-3	Sequence 3, Appli
	6	19	100.0	21	3	US-09-726-774-25	Sequence 25, Appl
	7	19	100.0	21	8	US-10-719-633-25	Sequence 25, Appl
	8	19	100.0	25	6	US-10-020-596-3	Sequence 3, Appli
	9	19	100.0	25	8	US-10-712-525-3	Sequence 3, Appli
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	11	19	100.0	26	3	US-09-736-151-4	Sequence 4, Appli
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	13	19	100.0	26	3	US-09-736-151-6	Sequence 6, Appli
	14	19	100.0	26	3	US-09-736-151-7	Sequence 7, Appli
	15	19	100.0	26	3	US-09-736-151-8	Sequence 8, Appli
	16	19	100.0	26	3	US-09-736-151-9	Sequence 9, Appli
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	28	19	100.0	26	10	US-10-973-162-4	Sequence 4, Appli
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c	37	19	100.0	59	8	US-10-329-624-4958	Sequence 4958, Ap
c	38	18	94.7	19	9	US-10-660-122-168	Sequence 168, App
c	39	18	94.7	19	9	US-10-660-122-234	Sequence 234, App
c	40	18	94.7	19	9	US-10-660-122-238	Sequence 238, App
c	41	18	94.7	19	9	US-10-660-122-240	Sequence 240, App
c	42	18	94.7	55	6	US-10-223-126-188	Sequence 188, App
c	43	18	94.7	55	15	US-11-070-519-188	Sequence 188, App
c	44	17.4	91.6	30	9	US-10-660-122-8	Sequence 8, Appli
c	45	16	84.2	20	11	US-10-831-286A-34358	Sequence 34358, A
c	46	15.4	81.1	25	11	US-10-933-982-5997	Sequence 5997, Ap
	47	14.4	75.8	19	11	US-10-310-914A-1106917	Sequence 1106917,
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c	49	14.2	74.7	24	11	US-10-310-914A-267576	Sequence 267576,
	50	14.2	74.7	25	8	US-10-719-956-527124	Sequence 527124,
	51	14.2	74.7	25	8	US-10-719-956-528344	Sequence 528344,
	52	14.2	74.7	25	13	US-11-036-317-93252	Sequence 93252, A
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c	54	14.2	74.7	25	16	US-11-136-527-345598	Sequence 345598,
	55	14	73.7	15	10	US-10-697-802A-118	Sequence 118, App
	56	14	73.7	16	10	US-10-697-802A-119	Sequence 119, App
	57	14	73.7	17	10	US-10-697-802A-123	Sequence 123, App
	58	14	73.7	18	10	US-10-697-802A-124	Sequence 124, App
	59	14	73.7	19	10	US-10-697-802A-132	Sequence 132, App
	60	14	73.7	20	10	US-10-697-802A-133	Sequence 133, App

ALIGNMENTS

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RESULT 1
US-10-085-134A-2
; Sequence 2, Application US/10085134A
; Publication No. US20030124545A1
; GENERAL INFORMATION:
;  APPLICANT: Rothman, Richard
;  APPLICANT:  Yang, Samuel
;  APPLICANT:  Lin, Shin
;  APPLICANT:  Kelen, Gabor
;  TITLE OF INVENTION: Quantitative Assay for the Simultaneous Detection and Speciation of
;  TITLE OF INVENTION:  Bacterial Infections
;  FILE REFERENCE: 001107.00234
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;  CURRENT APPLICATION NUMBER: US/10/085,134A
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: 60/272,642
;  PRIOR FILING DATE: 2001-03-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-085-134A-2

  Query Match             100.0%;  Score 19;  DB 7;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
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Db          1 TGCGGGACTTAACCCAACA 19


RESULT 2
US-10-085-134A-8/c
; Sequence 8, Application US/10085134A
; Publication No. US20030124545A1
; GENERAL INFORMATION:
;  APPLICANT: Rothman, Richard
;  APPLICANT:  Yang, Samuel
;  APPLICANT:  Lin, Shin
;  APPLICANT:  Kelen, Gabor
;  TITLE OF INVENTION: Quantitative Assay for the Simultaneous Detection and Speciation of
;  TITLE OF INVENTION:  Bacterial Infections
;  FILE REFERENCE: 001107.00234
;  CURRENT APPLICATION NUMBER: US/10/085,134A
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: 60/272,642
;  PRIOR FILING DATE: 2001-03-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-085-134A-8

  Query Match             100.0%;  Score 19;  DB 7;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
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Db         19 TGCGGGACTTAACCCAACA 1


RESULT 3
US-10-743-384-2
; Sequence 2, Application US/10743384
; Publication No. US20040235010A1
; GENERAL INFORMATION:
;  APPLICANT: Rothman, Richard
;  APPLICANT:  Yang, Samuel
;  APPLICANT:  Lin, Shin
;  APPLICANT:  Kelen, Gabor
;  TITLE OF INVENTION: Quantitative Assay for the Simultaneous Detection and Speciation of
;  TITLE OF INVENTION:  Bacterial Infections
;  FILE REFERENCE: 001107.00234
;  CURRENT APPLICATION NUMBER: US/10/743,384
;  CURRENT FILING DATE:  2003-12-23
;  PRIOR APPLICATION NUMBER: US/10/085,134A
;  PRIOR FILING DATE: 2002-03-01
;  PRIOR APPLICATION NUMBER: 60/272,642
;  PRIOR FILING DATE: 2001-03-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 19
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;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-743-384-2

  Query Match             100.0%;  Score 19;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          1 TGCGGGACTTAACCCAACA 19


RESULT 4
US-10-743-384-8/c
; Sequence 8, Application US/10743384
; Publication No. US20040235010A1
; GENERAL INFORMATION:
;  APPLICANT: Rothman, Richard
;  APPLICANT:  Yang, Samuel
;  APPLICANT:  Lin, Shin
;  APPLICANT:  Kelen, Gabor
;  TITLE OF INVENTION: Quantitative Assay for the Simultaneous Detection and Speciation of
;  TITLE OF INVENTION:  Bacterial Infections
;  FILE REFERENCE: 001107.00234
;  CURRENT APPLICATION NUMBER: US/10/743,384
;  CURRENT FILING DATE:  2003-12-23
;  PRIOR APPLICATION NUMBER: US/10/085,134A
;  PRIOR FILING DATE: 2002-03-01
;  PRIOR APPLICATION NUMBER: 60/272,642
;  PRIOR FILING DATE: 2001-03-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-743-384-8

  Query Match             100.0%;  Score 19;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
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Db         19 TGCGGGACTTAACCCAACA 1


RESULT 5
US-10-233-223-3
; Sequence 3, Application US/10233223
; Publication No. US20030105320A1
; GENERAL INFORMATION:
;  APPLICANT: Becker, Michael M.
;  APPLICANT:  Nelson, No. US20030105320A1man C.
;  TITLE OF INVENTION: Affinity-Shifted Probes for Quantifying
;  TITLE OF INVENTION:  Analyte Polynucleotides
;  FILE REFERENCE: GP129-03.UT
;  CURRENT APPLICATION NUMBER: US/10/233,223
;  CURRENT FILING DATE:  2002-08-30
;  PRIOR APPLICATION NUMBER: 60/316,770
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: 60/368,072
;  PRIOR FILING DATE: 2002-03-26
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: E. coli
US-10-233-223-3

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  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db          1 TGCGGGACTTAACCCAACA 19


RESULT 6
US-09-726-774-25
; Sequence 25, Application US/09726774
; Patent No. US20020082226A1
; GENERAL INFORMATION:
;  APPLICANT: Iversen, Patrick L.
;  TITLE OF INVENTION: Antisense Antibacterial Method and
;  TITLE OF INVENTION:  Composition
;  FILE REFERENCE: 0450-0032.30
;  CURRENT APPLICATION NUMBER: US/09/726,774
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 60/168,150
;  PRIOR FILING DATE: 1999-11-29
;  NUMBER OF SEQ ID NOS: 139
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense oligomer
US-09-726-774-25

  Query Match             100.0%;  Score 19;  DB 3;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db          2 TGCGGGACTTAACCCAACA 20


RESULT 7
US-10-719-633-25
; Sequence 25, Application US/10719633
; Publication No. US20040137485A1
; GENERAL INFORMATION:
;  APPLICANT: Iversen, Patrick L.
;  TITLE OF INVENTION: Antisense Antibacterial Method and
;  TITLE OF INVENTION:  Composition
;  FILE REFERENCE: 0450-0032.30
;  CURRENT APPLICATION NUMBER: US/10/719,633
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US/09/726,774
;  PRIOR FILING DATE: 2000-11-29
;  PRIOR APPLICATION NUMBER: US 60/168,150
;  PRIOR FILING DATE: 1999-11-29
;  NUMBER OF SEQ ID NOS: 139
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense oligomer
US-10-719-633-25

  Query Match             100.0%;  Score 19;  DB 8;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.8;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db          2 TGCGGGACTTAACCCAACA 20


RESULT 8
US-10-020-596-3
; Sequence 3, Application US/10020596
; Publication No. US20020164614A1
; GENERAL INFORMATION:
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;  APPLICANT: BECKER, Michael M.
;  TITLE OF INVENTION: METHOD AND KIT FOR ENHANCING THE ASSOCIATION RATES OF POLYNUCLEOTIDES
;  FILE REFERENCE: GP123-02.UT
;  CURRENT APPLICATION NUMBER: US/10/020,596
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: 60/255,535
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-020-596-3

  Query Match             100.0%;  Score 19;  DB 6;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
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Db          6 TGCGGGACTTAACCCAACA 24


RESULT 9
US-10-712-525-3
; Sequence 3, Application US/10712525
; Publication No. US20040077014A1
; GENERAL INFORMATION:
;  APPLICANT: BECKER, Michael M.
;  TITLE OF INVENTION: METHOD AND KIT FOR ENHANCING THE ASSOCIATION RATES OF POLYNUCLEOTIDES
;  FILE REFERENCE: GP123-02.UT
;  CURRENT APPLICATION NUMBER: US/10/712,525
;  CURRENT FILING DATE:  2200-11-01
;  PRIOR APPLICATION NUMBER: US/10/020,596
;  PRIOR FILING DATE: 2001-12-07
;  PRIOR APPLICATION NUMBER: 60/255,535
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-712-525-3

  Query Match             100.0%;  Score 19;  DB 8;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
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Db          6 TGCGGGACTTAACCCAACA 24


RESULT 10
US-10-660-122-10/c
; Sequence 10, Application US/10660122
; Publication No. US20040219517A1
; GENERAL INFORMATION:
;  APPLICANT: Ecker, David J.
;  APPLICANT:  Griffey, Richard H.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Hofstadler, Steven
;  APPLICANT:  McNeil, John
;  APPLICANT:  Crooke, Stanley T.
;  TITLE OF INVENTION: Methods For Rapid Identification Of Pathogens In Humans And Animals
;  FILE REFERENCE: IBIS0061-100
;  CURRENT APPLICATION NUMBER: US/10/660,122
;  CURRENT FILING DATE:  2003-09-11
;  PRIOR APPLICATION NUMBER: 10/323,233
;  PRIOR FILING DATE: 2002-12-18
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;  PRIOR APPLICATION NUMBER: 09/798,007
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/431,319
;  PRIOR FILING DATE: 2002-12-06
;  PRIOR APPLICATION NUMBER: 60/443,443
;  PRIOR FILING DATE: 2003-01-29
;  PRIOR APPLICATION NUMBER: 60/443,788
;  PRIOR FILING DATE: 2003-01-30
;  PRIOR APPLICATION NUMBER: 60/447,529
;  PRIOR FILING DATE: 2003-02-14
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR Primer
US-10-660-122-10

  Query Match             100.0%;  Score 19;  DB 9;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2


RESULT 11
US-09-736-151-4
; Sequence 4, Application US/09736151
; Patent No. US20020081586A1
; GENERAL INFORMATION:
;  APPLICANT: LAAYOUN, ALI
;  APPLICANT:  MENOU, LIONEL
;  APPLICANT:  TORA, CHRISTELLE
;  APPLICANT:  BANERJEE, ALOKE R.
;  APPLICANT:  BECKER, MICHAEL M.
;  APPLICANT:  BROWNE, KENNETH A.
;  APPLICANT:  FRIEDENBERG, MATTHEW C.
;  APPLICANT:  HAJJAR, FRED F.
;  TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
;  FILE REFERENCE: 104959
;  CURRENT APPLICATION NUMBER: US/09/736,151
;  CURRENT FILING DATE:  2000-12-15
;  PRIOR APPLICATION NUMBER: US 60/172,136
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 26
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-736-151-4

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
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Db          7 TGCGGGACTTAACCCAACA 25


RESULT 12
US-09-736-151-5
; Sequence 5, Application US/09736151
; Patent No. US20020081586A1
; GENERAL INFORMATION:
;  APPLICANT: LAAYOUN, ALI
;  APPLICANT:  MENOU, LIONEL
;  APPLICANT:  TORA, CHRISTELLE
;  APPLICANT:  BANERJEE, ALOKE R.
```

```
;  APPLICANT:  BECKER, MICHAEL M.
;  APPLICANT:  BROWNE, KENNETH A.
;  APPLICANT:  FRIEDENBERG, MATTHEW C.
;  APPLICANT:  HAJJAR, FRED F.
;  TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
;  FILE REFERENCE: 104959
;  CURRENT APPLICATION NUMBER: US/09/736,151
;  CURRENT FILING DATE:  2000-12-15
;  PRIOR APPLICATION NUMBER: US 60/172,136
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 26
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:primer ; the
;   OTHER INFORMATION: phosphate between nucleotides at positions 16 and
;   OTHER INFORMATION: 17  is a thiophosphate
US-09-736-151-5

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 13
US-09-736-151-6
; Sequence 6, Application US/09736151
; Patent No. US20020081586A1
; GENERAL INFORMATION:
;  APPLICANT: LAAYOUN, ALI
;  APPLICANT:  MENOU, LIONEL
;  APPLICANT:  TORA, CHRISTELLE
;  APPLICANT:  BANERJEE, ALOKE R.
;  APPLICANT:  BECKER, MICHAEL M.
;  APPLICANT:  BROWNE, KENNETH A.
;  APPLICANT:  FRIEDENBERG, MATTHEW C.
;  APPLICANT:  HAJJAR, FRED F.
;  TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
;  FILE REFERENCE: 104959
;  CURRENT APPLICATION NUMBER: US/09/736,151
;  CURRENT FILING DATE:  2000-12-15
;  PRIOR APPLICATION NUMBER: US 60/172,136
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 26
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:primer ; the
;   OTHER INFORMATION: phosphate at the 3' end is a terminal
;   OTHER INFORMATION: thiophosphate
US-09-736-151-6

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 14
US-09-736-151-7
; Sequence 7, Application US/09736151
; Patent No. US20020081586A1
; GENERAL INFORMATION:
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;  APPLICANT: LAAYOUN, ALI
;  APPLICANT:  MENOU, LIONEL
;  APPLICANT:  TORA, CHRISTELLE
;  APPLICANT:  BANERJEE, ALOKE R.
;  APPLICANT:  BECKER, MICHAEL M.
;  APPLICANT:  BROWNE, KENNETH A.
;  APPLICANT:  FRIEDENBERG, MATTHEW C.
;  APPLICANT:  HAJJAR, FRED F.
;  TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
;  FILE REFERENCE: 104959
;  CURRENT APPLICATION NUMBER: US/09/736,151
;  CURRENT FILING DATE:  2000-12-15
;  PRIOR APPLICATION NUMBER: US 60/172,136
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 26
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:primer ; the
;   OTHER INFORMATION: phosphate between the two nucleotides at position
;   OTHER INFORMATION: 16 and 17 is a thiophosphate
US-09-736-151-7

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   84.2%;  Pred. No. 5.9;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              :|||||||::|||||||||
Db          7 UGCGGGACUUAACCCAACA 25


RESULT 15
US-09-736-151-8
; Sequence 8, Application US/09736151
; Patent No. US20020081586A1
; GENERAL INFORMATION:
;  APPLICANT: LAAYOUN, ALI
;  APPLICANT:  MENOU, LIONEL
;  APPLICANT:  TORA, CHRISTELLE
;  APPLICANT:  BANERJEE, ALOKE R.
;  APPLICANT:  BECKER, MICHAEL M.
;  APPLICANT:  BROWNE, KENNETH A.
;  APPLICANT:  FRIEDENBERG, MATTHEW C.
;  APPLICANT:  HAJJAR, FRED F.
;  TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
;  FILE REFERENCE: 104959
;  CURRENT APPLICATION NUMBER: US/09/736,151
;  CURRENT FILING DATE:  2000-12-15
;  PRIOR APPLICATION NUMBER: US 60/172,136
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 26
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:primer ; the
;   OTHER INFORMATION: phosphate at the 3' end is a terminal
;   OTHER INFORMATION: thiophosphate
US-09-736-151-8

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   84.2%;  Pred. No. 5.9;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              :|||||||::|||||||||
Db          7 UGCGGGACUUAACCCAACA 25


RESULT 16
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US-09-736-151-9
; Sequence 9, Application US/09736151
; Patent No. US20020081586A1
; GENERAL INFORMATION:
;  APPLICANT: LAAYOUN, ALI
;  APPLICANT:  MENOU, LIONEL
;  APPLICANT:  TORA, CHRISTELLE
;  APPLICANT:  BANERJEE, ALOKE R.
;  APPLICANT:  BECKER, MICHAEL M.
;  APPLICANT:  BROWNE, KENNETH A.
;  APPLICANT:  FRIEDENBERG, MATTHEW C.
;  APPLICANT:  HAJJAR, FRED F.
;  TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
;  FILE REFERENCE: 104959
;  CURRENT APPLICATION NUMBER: US/09/736,151
;  CURRENT FILING DATE:  2000-12-15
;  PRIOR APPLICATION NUMBER: US 60/172,136
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 26
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-736-151-9

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   84.2%;  Pred. No. 5.9;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              :|||||||::|||||||||
Db          7 UGCGGGACUUAACCCAACA 25


RESULT 17
US-09-808-558-1
; Sequence 1, Application US/09808558
; Publication No. US20030036058A1
;   GENERAL INFORMATION:
;        APPLICANT: Becker, Michael M.
;                   Majlessi, Mehrdad
;        TITLE OF INVENTION: METHODS FOR DETECTING AND
;                            AMPLIFYING NUCLEIC ACID SEQUENCES USING MODIFIED
;                            OLIGONUCLEOTIDES HAVING INCREASED TARGET SPECIFIC TM
;        NUMBER OF SEQUENCES: 2
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Gen-Probe Incorporated
;             STREET: 10210 Genetic Center Drive
;             CITY: San Diego
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92121
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/808,558
;             FILING DATE: 14-Mar-2001
;             CLASSIFICATION:
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/893,300
;             FILING DATE: 15-JUL-1997
;             APPLICATION NUMBER: 60/021,818
;             FILING DATE: 15-JUL-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Cappellari, Charles B
;             REGISTRATION NUMBER: 40,937
;             REFERENCE/DOCKET NUMBER: CHE7B-P01A01
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619-410-8927
;             TELEFAX: 619-410-8928
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;             TELEX:
;    INFORMATION FOR SEQ ID NO: 1:
;         SEQUENCE CHARACTERISTICS:
;             LENGTH: 26 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-808-558-1

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 18
US-09-808-558-2/c
; Sequence 2, Application US/09808558
; Publication No. US20030036058A1
;   GENERAL INFORMATION:
;         APPLICANT: Becker, Michael M.
;                    Majlessi, Mehrdad
;         TITLE OF INVENTION: METHODS FOR DETECTING AND
;                             AMPLIFYING NUCLEIC ACID SEQUENCES USING MODIFIED
;                             OLIGONUCLEOTIDES HAVING INCREASED TARGET SPECIFIC TM
;         NUMBER OF SEQUENCES: 2
;         CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Gen-Probe Incorporated
;             STREET: 10210 Genetic Center Drive
;             CITY: San Diego
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92121
;         COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;         CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/808,558
;             FILING DATE: 14-Mar-2001
;             CLASSIFICATION:
;         PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/893,300
;             FILING DATE: 15-JUL-1997
;             APPLICATION NUMBER: 60/021,818
;             FILING DATE: 15-JUL-1996
;         ATTORNEY/AGENT INFORMATION:
;             NAME: Cappellari, Charles B
;             REGISTRATION NUMBER: 40,937
;             REFERENCE/DOCKET NUMBER: CHE7B-P01A01
;         TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619-410-8927
;             TELEFAX: 619-410-8928
;             TELEX:
;    INFORMATION FOR SEQ ID NO: 2:
;         SEQUENCE CHARACTERISTICS:
;             LENGTH: 26 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-808-558-2

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2
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RESULT 19
US-10-020-596-1
; Sequence 1, Application US/10020596
; Publication No. US20020164614A1
; GENERAL INFORMATION:
;  APPLICANT: BECKER, Michael M.
;  TITLE OF INVENTION: METHOD AND KIT FOR ENHANCING THE ASSOCIATION RATES OF POLYNUCLEOTIDES
;  FILE REFERENCE: GP123-02.UT
;  CURRENT APPLICATION NUMBER: US/10/020,596
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: 60/255,535
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 26
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-020-596-1

  Query Match             100.0%;  Score 19;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 20
US-10-020-596-2/c
; Sequence 2, Application US/10020596
; Publication No. US20020164614A1
; GENERAL INFORMATION:
;  APPLICANT: BECKER, Michael M.
;  TITLE OF INVENTION: METHOD AND KIT FOR ENHANCING THE ASSOCIATION RATES OF POLYNUCLEOTIDES
;  FILE REFERENCE: GP123-02.UT
;  CURRENT APPLICATION NUMBER: US/10/020,596
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: 60/255,535
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 26
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-020-596-2

  Query Match             100.0%;  Score 19;  DB 6;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2


Search completed: July 26, 2006, 17:25:39
Job time : 623.366 secs
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SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10743384 and Search Result us-10-743-384-2.szlm60.rni.

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                    GenCore version 5.1.9
                Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         July 26, 2006, 15:54:56 ; Search time 70.439 Seconds
                                          (without alignments)
                                          504.707 Million cell updates/sec

Title:          US-10-743-384-2
Perfect score:  19
Sequence:       1 tgcgggacttaacccaaca 19

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1403666 seqs, 935554401 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Database :        Issued_Patents_NA:*
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                 4:  /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES

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Result              Query
   No.    Score     Match  Length  DB  ID                          Description
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 c   2       19   100.0      19   3  US-10-085-134A-8             Sequence 8, Appli
     3       19   100.0      21   3  US-09-726-774-25             Sequence 25, Appl
     4       19   100.0      26   2  US-08-478-221-5              Sequence 5, Appli
 c   5       19   100.0      26   2  US-08-478-221-6              Sequence 6, Appli
     6       19   100.0      26   2  US-08-478-221-11             Sequence 11, Appl
 c   7       19   100.0      26   2  US-08-478-221-12             Sequence 12, Appl
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	10	19	100.0	26	3	US-09-094-139-1	Sequence 1, Appli
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	15	19	100.0	26	3	US-09-736-151-5	Sequence 5, Appli
	16	19	100.0	26	3	US-09-736-151-6	Sequence 6, Appli
	17	19	100.0	26	3	US-09-736-151-7	Sequence 7, Appli
	18	19	100.0	26	3	US-09-736-151-8	Sequence 8, Appli
	19	19	100.0	26	3	US-09-736-151-9	Sequence 9, Appli
c	20	19	100.0	26	3	US-09-523-237B-1	Sequence 1, Appli
	21	19	100.0	26	3	US-09-523-237B-2	Sequence 2, Appli
	22	19	100.0	26	3	US-09-523-237B-3	Sequence 3, Appli
	23	19	100.0	26	3	US-09-523-237B-4	Sequence 4, Appli
	24	19	100.0	26	3	US-09-523-237B-5	Sequence 5, Appli
	25	19	100.0	26	3	US-09-523-237B-6	Sequence 6, Appli
	26	19	100.0	26	3	US-09-523-237B-7	Sequence 7, Appli
c	27	19	100.0	26	3	US-09-523-237B-8	Sequence 8, Appli
c	28	19	100.0	26	3	US-09-523-237B-9	Sequence 9, Appli
	29	19	100.0	26	3	US-09-523-237B-10	Sequence 10, Appl
	30	19	100.0	26	3	US-09-523-237B-11	Sequence 11, Appl
c	31	19	100.0	59	3	US-08-956-171E-4958	Sequence 4958, Ap
c	32	19	100.0	59	3	US-08-781-986A-4958	Sequence 4958, Ap
c	33	14	73.7	18	3	US-09-073-465-12	Sequence 12, Appl
	34	14	73.7	18	3	US-09-073-465-13	Sequence 13, Appl
c	35	14	73.7	22	2	US-08-244-269-46	Sequence 46, Appl
c	36	14	73.7	22	2	US-07-923-871C-26	Sequence 26, Appl
c	37	14	73.7	22	3	US-09-634-960A-38	Sequence 38, Appl
c	38	14	73.7	22	7	PCT-US91-01574-26	Sequence 26, Appl
	39	14	73.7	25	2	US-08-743-637B-272	Sequence 272, App
	40	13.4	70.5	22	3	US-09-700-486-5	Sequence 5, Appli
	41	13.2	69.5	51	3	US-09-989-002-49	Sequence 49, Appl
	42	13	68.4	21	3	US-09-726-774-28	Sequence 28, Appl
c	43	12.8	67.4	18	10	5180819-5	Patent No. 5180819
	44	12.8	67.4	18	10	5180819-8	Patent No. 5180819
	45	12.8	67.4	20	3	US-09-357-071-22	Sequence 22, Appl
	46	12.8	67.4	26	3	US-09-989-002-23	Sequence 23, Appl
	47	12.2	64.2	50	3	US-10-131-827-4842	Sequence 4842, Ap
	48	12.2	64.2	50	5	US-10-131-831-4842	Sequence 4842, Ap
	49	12	63.2	28	3	US-09-549-848B-73	Sequence 73, Appl
	50	12	63.2	28	3	US-09-688-069-73	Sequence 73, Appl
	51	12	63.2	33	3	US-09-609-133F-4	Sequence 4, Appli
c	52	12	63.2	40	3	US-09-495-066-7	Sequence 7, Appli
c	53	11.8	62.1	22	3	US-08-714-918-109	Sequence 109, App
c	54	11.8	62.1	22	3	US-09-265-315-109	Sequence 109, App
c	55	11.8	62.1	22	3	US-09-265-315-109	Sequence 109, App
c	56	11.8	62.1	22	3	US-09-266-417-109	Sequence 109, App
c	57	11.8	62.1	22	3	US-09-528-709-109	Sequence 109, App
c	58	11.8	62.1	22	3	US-09-527-745-109	Sequence 109, App
c	59	11.8	62.1	50	3	US-10-131-827-1522	Sequence 1522, Ap
c	60	11.8	62.1	50	5	US-10-131-831-1522	Sequence 1522, Ap

ALIGNMENTS

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RESULT 1
US-10-085-134A-2
; Sequence 2, Application US/10085134A
; Patent No. 6699670
; GENERAL INFORMATION:
;  APPLICANT: Rothman, Richard
;  APPLICANT:  Yang, Samuel
;  APPLICANT:  Lin, Shin
;  APPLICANT:  Kelen, Gabor
;  TITLE OF INVENTION: Quantitative Assay for the Simultaneous Detection and Speciation of
;  TITLE OF INVENTION:  Bacterial Infections
;  FILE REFERENCE: 001107.00234
;  CURRENT APPLICATION NUMBER: US/10/085,134A
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: 60/272,642
;' PRIOR FILING DATE: 2001-03-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 2
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-085-134A-2

  Query Match             100.0%;  Score 19;  DB 3;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.29;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          1 TGCGGGACTTAACCCAACA 19


RESULT 2
US-10-085-134A-8/c
; Sequence 8, Application US/10085134A
; Patent No. 6699670
; GENERAL INFORMATION:
;  APPLICANT: Rothman, Richard
;  APPLICANT:  Yang, Samuel
;  APPLICANT:  Lin, Shin
;  APPLICANT:  Kelen, Gabor
;  TITLE OF INVENTION: Quantitative Assay for the Simultaneous Detection and Speciation of
;  TITLE OF INVENTION:  Bacterial Infections
;  FILE REFERENCE: 001107.00234
;  CURRENT APPLICATION NUMBER: US/10/085,134A
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: 60/272,642
;  PRIOR FILING DATE: 2001-03-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
US-10-085-134A-8

  Query Match             100.0%;  Score 19;  DB 3;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.29;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db         19 TGCGGGACTTAACCCAACA 1


RESULT 3
US-09-726-774-25
; Sequence 25, Application US/09726774
; Patent No. 6677153
; GENERAL INFORMATION:
;  APPLICANT: Iversen, Patrick L.
;  TITLE OF INVENTION: Antisense Antibacterial Method and
;  TITLE OF INVENTION:  Composition
;  FILE REFERENCE: 0450-0032.30
;  CURRENT APPLICATION NUMBER: US/09/726,774
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER: US 60/168,150
;  PRIOR FILING DATE: 1999-11-29
;  NUMBER OF SEQ ID NOS: 139
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antisense oligomer
US-09-726-774-25

  Query Match             100.0%;  Score 19;  DB 3;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.3;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
```

```
              ||||||||||||||||||
Db          2 TGCGGGACTTAACCCAACA 20


RESULT 4
US-08-478-221-5
; Sequence 5, Application US/08478221
; Patent No. 5731148
;  GENERAL INFORMATION:
;    APPLICANT:  Michael Becker
;    APPLICANT:  No. 5731148man C. Nelson
;    TITLE OF INVENTION:  ADDUCT PROTECTION ASSAY
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,221
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:            No. 5731148e
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heber, Sheldon O.
;      REGISTRATION NUMBER:  38,179
;      REFERENCE/DOCKET NUMBER:  209/190
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  nucleic acid
US-08-478-221-5

  Query Match            100.0%;  Score 19;  DB 2;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 0.31;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 5
US-08-478-221-6/c
; Sequence 6, Application US/08478221
; Patent No. 5731148
;  GENERAL INFORMATION:
;    APPLICANT:  Michael Becker
;    APPLICANT:  No. 5731148man C. Nelson
;    TITLE OF INVENTION:  ADDUCT PROTECTION ASSAY
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
```

```
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,221
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:           No. 5731148e
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heber, Sheldon O.
;      REGISTRATION NUMBER:  38,179
;      REFERENCE/DOCKET NUMBER:  209/190
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  nucleic acid
US-08-478-221-6

  Query Match             100.0%;  Score 19;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2


RESULT 6
US-08-478-221-11
; Sequence 11, Application US/08478221
; Patent No. 5731148
;  GENERAL INFORMATION:
;    APPLICANT:  Michael Becker
;    APPLICANT:  No. 5731148man C. Nelson
;    TITLE OF INVENTION:  ADDUCT PROTECTION ASSAY
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,221
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:           No. 5731148e
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heber, Sheldon O.
;      REGISTRATION NUMBER:  38,179
;      REFERENCE/DOCKET NUMBER:  209/190
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
```

```
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  nucleic acid
US-08-478-221-11

  Query Match            100.0%;  Score 19;  DB 2;  Length 26;
  Best Local Similarity   84.2%;  Pred. No. 0.31;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              :|||||||::|||||||||
Db          7 UGCGGGACUUAACCCAACA 25


RESULT 7
US-08-478-221-12/c
; Sequence 12, Application US/08478221
; Patent No. 5731148
;  GENERAL INFORMATION:
;    APPLICANT:  Michael Becker
;    APPLICANT:  No. 5731148man C. Nelson
;    TITLE OF INVENTION:  ADDUCT PROTECTION ASSAY
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,221
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:            No. 5731148e
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heber, Sheldon O.
;      REGISTRATION NUMBER:  38,179
;      REFERENCE/DOCKET NUMBER:  209/190
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  nucleic acid
US-08-478-221-12

  Query Match            100.0%;  Score 19;  DB 2;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 0.31;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2
```

```
RESULT 8
US-08-475-334-1
; Sequence 1, Application US/08475334
; Patent No. 5879885
;  GENERAL INFORMATION:
;    APPLICANT:  Becker, Michael M.
;    TITLE OF INVENTION:  MICELLE PROTECTION ASSAY
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Gen-Probe Incorporated
;      STREET:  9880 Campus Point Drive
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,334
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fisher, Carlos A
;      REGISTRATION NUMBER:  36,510
;      REFERENCE/DOCKET NUMBER:  GP94009
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-535-2807
;      TELEFAX:  619-546-7929
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-475-334-1

  Query Match             100.0%;  Score 19;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 9
US-08-475-334-2/c
; Sequence 2, Application US/08475334
; Patent No. 5879885
;  GENERAL INFORMATION:
;    APPLICANT:  Becker, Michael M.
;    TITLE OF INVENTION:  MICELLE PROTECTION ASSAY
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Geh-Probe Incorporated
;      STREET:  9880 Campus Point Drive
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,334
;      FILING DATE:
;      CLASSIFICATION:  435
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fisher, Carlos A
;      REGISTRATION NUMBER:  36,510
;      REFERENCE/DOCKET NUMBER:  GP94009
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-535-2807
;      TELEFAX:  619-546-7929
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-475-334-2

  Query Match             100.0%;  Score 19;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2


RESULT 10
US-09-094-139-1
; Sequence 1, Application US/09094139
; Patent No. 6059561
;  GENERAL INFORMATION:
;    APPLICANT:  Becker, Michael M.
;    TITLE OF INVENTION:  MICELLE PROTECTION ASSAY
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Gen-Probe Incorporated
;      STREET:  9880 Campus Point Drive
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/094,139
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,334
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fisher, Carlos A
;      REGISTRATION NUMBER:  36,510
;      REFERENCE/DOCKET NUMBER:  GP94009
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-535-2807
;      TELEFAX:  619-546-7929
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-094-139-1

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
```

```
                  ||||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 11
US-09-094-139-2/c
; Sequence 2, Application US/09094139
; Patent No. 6059561
;  GENERAL INFORMATION:
;    APPLICANT:  Becker, Michael M.
;    TITLE OF INVENTION:  MICELLE PROTECTION ASSAY
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Gen-Probe Incorporated
;      STREET:  9880 Campus Point Drive
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/094,139
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,334
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fisher, Carlos A
;      REGISTRATION NUMBER:  36,510
;      REFERENCE/DOCKET NUMBER:  GP94009
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-535-2807
;      TELEFAX:  619-546-7929
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-094-139-2

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2


RESULT 12
US-08-893-300-1
; Sequence 1, Application US/08893300
; Patent No. 6130038
;  GENERAL INFORMATION:
;    APPLICANT:  Becker, Michael M.
;    APPLICANT:  Majlessi, Mehrdad
;    TITLE OF INVENTION:  METHODS FOR DETECTING AND
;    TITLE OF INVENTION:  AMPLIFYING NUCLEIC ACID SEQUENCES USING MODIFIED
;    TITLE OF INVENTION:  OLIGONUCLEOTIDES HAVING INCREASED TARGET SPECIFIC TM
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Gen-Probe Incorporated
;      STREET:  10210 Genetic Center Drive
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
```

```
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/893,300
;      FILING DATE:  15-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/021,818
;      FILING DATE:  15-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cappellari, Charles B
;      REGISTRATION NUMBER:  40,937
;      REFERENCE/DOCKET NUMBER:  CHE7B-P01A01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-410-8927
;      TELEFAX:  619-410-8928
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-893-300-1

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 13
US-08-893-300-2/c
; Sequence 2, Application US/08893300
; Patent No. 6130038
;  GENERAL INFORMATION:
;    APPLICANT:  Becker, Michael M.
;    APPLICANT:  Majlessi, Mehrdad
;    TITLE OF INVENTION:  METHODS FOR DETECTING AND
;    TITLE OF INVENTION:  AMPLIFYING NUCLEIC ACID SEQUENCES USING MODIFIED
;    TITLE OF INVENTION:  OLIGONUCLEOTIDES HAVING INCREASED TARGET SPECIFIC TM
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Gen-Probe Incorporated
;      STREET:  10210 Genetic Center Drive
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/893,300
;      FILING DATE:  15-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/021,818
;      FILING DATE:  15-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cappellari, Charles B
;      REGISTRATION NUMBER:  40,937
;      REFERENCE/DOCKET NUMBER:  CHE7B-P01A01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-410-8927
;      TELEFAX:  619-410-8928
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
```

```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-893-300-2

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2


RESULT 14
US-09-736-151-4
; Sequence 4, Application US/09736151
; Patent No. 6902891
; GENERAL INFORMATION:
;  APPLICANT: LAAYOUN, ALI
;  APPLICANT:  MENOU, LIONEL
;  APPLICANT:  TORA, CHRISTELLE
;  APPLICANT:  BANERJEE, ALOKE R.
;  APPLICANT:  BECKER, MICHAEL M.
;  APPLICANT:  BROWNE, KENNETH A.
;  APPLICANT:  FRIEDENBERG, MATTHEW C.
;  APPLICANT:  HAJJAR, FRED F.
;  TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
;  FILE REFERENCE: 104959
;  CURRENT APPLICATION NUMBER: US/09/736,151
;  CURRENT FILING DATE:  2000-12-15
;  PRIOR APPLICATION NUMBER: US 60/172,136
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 26
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-736-151-4

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 15
US-09-736-151-5
; Sequence 5, Application US/09736151
; Patent No. 6902891
; GENERAL INFORMATION:
;  APPLICANT: LAAYOUN, ALI
;  APPLICANT:  MENOU, LIONEL
;  APPLICANT:  TORA, CHRISTELLE
;  APPLICANT:  BANERJEE, ALOKE R.
;  APPLICANT:  BECKER, MICHAEL M.
;  APPLICANT:  BROWNE, KENNETH A.
;  APPLICANT:  FRIEDENBERG, MATTHEW C.
;  APPLICANT:  HAJJAR, FRED F.
;  TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
;  FILE REFERENCE: 104959
;  CURRENT APPLICATION NUMBER: US/09/736,151
;  CURRENT FILING DATE:  2000-12-15
;  PRIOR APPLICATION NUMBER: US 60/172,136
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 26
;   TYPE: DNA
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:primer ; the
;   OTHER INFORMATION: phosphate between nucleotides at positions 16 and
;   OTHER INFORMATION: 17  is a thiophosphate
US-09-736-151-5

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 16
US-09-736-151-6
; Sequence 6, Application US/09736151
; Patent No. 6902891
; GENERAL INFORMATION:
;  APPLICANT: LAAYOUN, ALI
;  APPLICANT:  MENOU, LIONEL
;  APPLICANT:  TORA, CHRISTELLE
;  APPLICANT:  BANERJEE, ALOKE R.
;  APPLICANT:  BECKER, MICHAEL M.
;  APPLICANT:  BROWNE, KENNETH A.
;  APPLICANT:  FRIEDENBERG, MATTHEW C.
;  APPLICANT:  HAJJAR, FRED F.
;  TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
;  FILE REFERENCE: 104959
;  CURRENT APPLICATION NUMBER: US/09/736,151
;  CURRENT FILING DATE:  2000-12-15
;  PRIOR APPLICATION NUMBER: US 60/172,136
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 26
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:primer ; the
;   OTHER INFORMATION: phosphate at the 3' end is a terminal
;   OTHER INFORMATION: thiophosphate
US-09-736-151-6

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 17
US-09-736-151-7
; Sequence 7, Application US/09736151
; Patent No. 6902891
; GENERAL INFORMATION:
;  APPLICANT: LAAYOUN, ALI
;  APPLICANT:  MENOU, LIONEL
;  APPLICANT:  TORA, CHRISTELLE
;  APPLICANT:  BANERJEE, ALOKE R.
;  APPLICANT:  BECKER, MICHAEL M.
;  APPLICANT:  BROWNE, KENNETH A.
;  APPLICANT:  FRIEDENBERG, MATTHEW C.
;  APPLICANT:  HAJJAR, FRED F.
;  TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
;  FILE REFERENCE: 104959
;  CURRENT APPLICATION NUMBER: US/09/736,151
;  CURRENT FILING DATE:  2000-12-15
;  PRIOR APPLICATION NUMBER: US 60/172,136
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 26
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:primer ; the
;   OTHER INFORMATION: phosphate between the two nucleotides at position
;   OTHER INFORMATION: 16 and 17 is a thiophosphate
US-09-736-151-7

  Query Match            100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   84.2%;  Pred. No. 0.31;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              :||||||||::|||||||||
Db          7 UGCGGGACUUAACCCAACA 25


RESULT 18
US-09-736-151-8
; Sequence 8, Application US/09736151
; Patent No. 6902891
; GENERAL INFORMATION:
;  APPLICANT: LAAYOUN, ALI
;  APPLICANT:  MENOU, LIONEL
;  APPLICANT:  TORA, CHRISTELLE
;  APPLICANT:  BANERJEE, ALOKE R.
;  APPLICANT:  BECKER, MICHAEL M.
;  APPLICANT:  BROWNE, KENNETH A.
;  APPLICANT:  FRIEDENBERG, MATTHEW C.
;  APPLICANT:  HAJJAR, FRED F.
;  TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
;  FILE REFERENCE: 104959
;  CURRENT APPLICATION NUMBER: US/09/736,151
;  CURRENT FILING DATE:  2000-12-15
;  PRIOR APPLICATION NUMBER: US 60/172,136
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 26
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:primer ; the
;   OTHER INFORMATION: phosphate at the 3' end is a terminal
;   OTHER INFORMATION: thiophosphate
US-09-736-151-8

  Query Match            100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   84.2%;  Pred. No. 0.31;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              :||||||||::|||||||||
Db          7 UGCGGGACUUAACCCAACA 25


RESULT 19
US-09-736-151-9
; Sequence 9, Application US/09736151
; Patent No. 6902891
; GENERAL INFORMATION:
;  APPLICANT: LAAYOUN, ALI
;  APPLICANT:  MENOU, LIONEL
;  APPLICANT:  TORA, CHRISTELLE
;  APPLICANT:  BANERJEE, ALOKE R.
;  APPLICANT:  BECKER, MICHAEL M.
;  APPLICANT:  BROWNE, KENNETH A.
;  APPLICANT:  FRIEDENBERG, MATTHEW C.
;  APPLICANT:  HAJJAR, FRED F.
;  TITLE OF INVENTION: PROCESS FOR LABELING A NUCLEIC ACID
;  FILE REFERENCE: 104959
;  CURRENT APPLICATION NUMBER: US/09/736,151
```

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;  CURRENT FILING DATE:  2000-12-15
;  PRIOR APPLICATION NUMBER: US 60/172,136
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 26
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-736-151-9

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   84.2%;  Pred. No. 0.31;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              :|||||||::|||||||||
Db          7 UGCGGGACUUAACCCAACA 25


RESULT 20
US-09-523-237B-1/c
; Sequence 1, Application US/09523237B
; Patent No. 6903206
; GENERAL INFORMATION:
;  APPLICANT: Becker, Michael M.
;  APPLICANT:  Majlessi, Mehrdad
;  APPLICANT:  Brentano, Steven T.
;  TITLE OF INVENTION: Kits for Amplifying Nucleic Acid Sequences Using Modified
;  TITLE OF INVENTION:  Oligonucleotides
;  FILE REFERENCE: GP068-03.CN1
;  CURRENT APPLICATION NUMBER: US/09/523,237B
;  CURRENT FILING DATE:  2000-03-10
;  PRIOR APPLICATION NUMBER: 08/893,300
;  PRIOR FILING DATE: 1997-07-15
;  PRIOR APPLICATION NUMBER: 60/021,818
;  PRIOR FILING DATE: 1996-07-16
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 26
;   TYPE: DNA
;   ORGANISM: Escherichia coli
US-09-523-237B-1

  Query Match             100.0%;  Score 19;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.31;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2


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Job time : 70.439 secs
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SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10743384 and Search Result us-10-743-384-2.szlm60.rge.

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OM nucleic - nucleic search, using sw model

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Perfect score:  19
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      2455354

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Database :        GenEmbl:*
                 1:  gb_env:*
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                 8:  gb_sy:*
                 9:  gb_un:*
                 10:  gb_vi:*
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                 12:  gb_htg:*
                 13:  gb_in:*
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                 15:  gb_ba:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES
                 %
Result           Query
   No.    Score  Match Length DB  ID                          Description
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     1       19  100.0     19  2  CQ818165                    CQ818165 Sequence
     2       19  100.0     19  2  AR478754                    AR478754 Sequence
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c	3	19	100.0	19	2	AR478760	AR478760 Sequence
	4	19	100.0	21	2	AR452380	AR452380 Sequence
	5	19	100.0	21	2	AX201200	AX201200 Sequence
c	6	19	100.0	23	2	BD205810	BD205810 A method
c	7	19	100.0	23	2	AX010473	AX010473 Sequence
	8	19	100.0	25	2	AX463303	AX463303 Sequence
	9	19	100.0	26	2	AR112109	AR112109 Sequence
c	10	19	100.0	26	2	AR112110	AR112110 Sequence
	11	19	100.0	26	2	I93509	I93509 Sequence 5
c	12	19	100.0	26	2	I93510	I93510 Sequence 6
	13	19	100.0	26	2	I93515	I93515 Sequence 11
c	14	19	100.0	26	2	I93516	I93516 Sequence 12
	15	19	100.0	26	2	AR678434	AR678434 Sequence
	16	19	100.0	26	2	AR678435	AR678435 Sequence
	17	19	100.0	26	2	AR678436	AR678436 Sequence
	18	19	100.0	26	2	AR678437	AR678437 Sequence
	19	19	100.0	26	2	AR678438	AR678438 Sequence
	20	19	100.0	26	2	AR678439	AR678439 Sequence
c	21	19	100.0	26	2	AR680175	AR680175 Sequence
	22	19	100.0	26	2	AR680176	AR680176 Sequence
	23	19	100.0	26	2	AR680177	AR680177 Sequence
	24	19	100.0	26	2	AR680178	AR680178 Sequence
	25	19	100.0	26	2	AR680179	AR680179 Sequence
	26	19	100.0	26	2	AR680180	AR680180 Sequence
	27	19	100.0	26	2	AR680181	AR680181 Sequence
c	28	19	100.0	26	2	AR680182	AR680182 Sequence
c	29	19	100.0	26	2	AR680183	AR680183 Sequence
	30	19	100.0	26	2	AR680184	AR680184 Sequence
	31	19	100.0	26	2	AR680185	AR680185 Sequence
	32	19	100.0	26	2	AX166827	AX166827 Sequence
	33	19	100.0	26	2	AX166828	AX166828 Sequence
	34	19	100.0	26	2	AX166829	AX166829 Sequence
	35	19	100.0	26	2	AX166830	AX166830 Sequence
	36	19	100.0	26	2	AX166831	AX166831 Sequence
	37	19	100.0	26	2	AX166832	AX166832 Sequence
	38	19	100.0	26	2	AX463301	AX463301 Sequence
c	39	19	100.0	26	2	AX463302	AX463302 Sequence
c	40	19	100.0	51	2	CQ819522	CQ819522 Sequence
c	41	19	100.0	59	2	AR358840	AR358840 Sequence
c	42	19	100.0	59	2	AR540396	AR540396 Sequence
	43	17.4	91.6	33	2	BD140319	BD140319 Universal
c	44	17	89.5	23	2	BD205788	BD205788 A method
c	45	17	89.5	23	2	AX010451	AX010451 Sequence
c	46	14.4	75.8	60	2	CQ553680	CQ553680 Sequence
c	47	14	73.7	22	2	AR071559	AR071559 Sequence
c	48	14	73.7	22	2	I40288	I40288 Sequence 46
c	49	14	73.7	22	2	AR526803	AR526803 Sequence
	50	14	73.7	25	2	AR089513	AR089513 Sequence
	51	13.4	70.5	22	2	AR372759	AR372759 Sequence
	52	13.4	70.5	22	2	AX010413	AX010413 Sequence
	53	13.4	70.5	25	2	BD001703	BD001703 Compositi
	54	13.4	70.5	25	2	BD001716	BD001716 Method fo
	55	13.2	69.5	51	2	BD171631	BD171631 Method fo
	56	13.2	69.5	51	2	AR404984	AR404984 Sequence
	57	13.2	69.5	51	2	AX441330	AX441330 Sequence
c	58	13	68.4	13	2	CQ819524	CQ819524 Sequence
c	59	13	68.4	20	2	AX746436	AX746436 Sequence
	60	13	68.4	21	2	AR452382	AR452382 Sequence

ALIGNMENTS

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RESULT 1
CQ818165
LOCUS       CQ818165                  19 bp    DNA     linear   PAT 07-JUN-2004
DEFINITION  Sequence 2 from Patent WO2004044247.
ACCESSION   CQ818165
VERSION     CQ818165.1  GI:48426957
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Chaubron,F., Martin-Minvielle,A.C. and Groulon,S.
  TITLE     One step real-time rt pcr kits for the universal detection of
```

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            organisms in industrial products
  JOURNAL   Patent: WO 2004044247-A 2 27-MAY-2004;
            Genolife (FR)
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="#Description of artificial sequence:
                      oligonucleotide primer#"
ORIGIN

  Query Match             100.0%;  Score 19;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 7.6e+05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          1 TGCGGGACTTAACCCAACA 19


RESULT 2
AR478754
LOCUS       AR478754                  19 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 2 from patent US 6699670.
ACCESSION   AR478754
VERSION     AR478754.1  GI:47237474
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Rothman,R.E., Yang,S., Lin,S. and Kelen,G.D.
  TITLE     Quantitative assay for the simultaneous detection and speciation of
            bacterial infections
  JOURNAL   Patent: US 6699670-A 2 02-MAR-2004;
            The Johns Hopkins University; Baltimore, MD
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 19;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 7.6e+05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          1 TGCGGGACTTAACCCAACA 19


RESULT 3
AR478760/c
LOCUS       AR478760                  19 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 8 from patent US 6699670.
ACCESSION   AR478760
VERSION     AR478760.1  GI:47237480
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Rothman,R.E., Yang,S., Lin,S. and Kelen,G.D.
  TITLE     Quantitative assay for the simultaneous detection and speciation of
            bacterial infections
  JOURNAL   Patent: US 6699670-A 8 02-MAR-2004;
            The Johns Hopkins University; Baltimore, MD
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 19;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 7.6e+05;
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db         19 TGCGGGACTTAACCCAACA 1


RESULT 4
AR452380
LOCUS       AR452380                  21 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 25 from patent US 6677153.
ACCESSION   AR452380
VERSION     AR452380.1  GI:42684027
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Iversen,P.L.
  TITLE     Antisense antibacterial method and composition
  JOURNAL   Patent: US 6677153-A 25 13-JAN-2004;
            AVI BioPharma, Inc.; Covallis, OR
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 19;  DB 2;  Length 21;
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          2 TGCGGGACTTAACCCAACA 20


RESULT 5
AX201200
LOCUS       AX201200                  21 bp    DNA     linear   PAT 29-AUG-2001
DEFINITION  Sequence 25 from Patent WO0142457.
ACCESSION   AX201200
VERSION     AX201200.1  GI:15390952
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Iversen,P.L.
  TITLE     Antisense antibacterial method and composition
  JOURNAL   Patent: WO 0142457-A 25 14-JUN-2001;
            Avi Biopharma, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="antisense oligomer"
ORIGIN

  Query Match             100.0%;  Score 19;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 7.5e+05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          2 TGCGGGACTTAACCCAACA 20


RESULT 6
BD205810/c
LOCUS       BD205810                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  A method for detecting microorganisms in products.
ACCESSION   BD205810
VERSION     BD205810.1  GI:33015580
KEYWORDS    JP 2002514439-A/52.
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Gerbling,K.P., Lauter,F.R. and Grohmann,L.
  TITLE     A method for detecting microorganisms in products
  JOURNAL   Patent: JP 2002514439-A 52 21-MAY-2002;
            BIOINSIDE GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002514439-A/52
            PD   21-MAY-2002
            PF   10-MAY-1999 JP 2000548504
            PR   12-MAY-1998 DE 198 22 108.8
            PI   KLAUS PETER GERBLING,FRANK ROMAN LAUTER,LUTZ GROHMANN PC
            C12N15/09,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence: sonde
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 19;  DB 2;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2


RESULT 7
AX010473/c
LOCUS       AX010473                 23 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 52 from Patent WO9958713.
ACCESSION   AX010473
VERSION     AX010473.1  GI:9997316
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Grohmann,L., Gerbling,K.P. and Lauter,F.R.
  TITLE     Method for detecting microorganisms in products
  JOURNAL   Patent: WO 9958713-A 52 18-NOV-1999;
            GROHMANN LUTZ (DE); BIOINSIDE GMBH (DE); GERBLING KLAUS PETER (DE);
            LAUTER FRANK ROMAN (DE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Sonde"
ORIGIN

  Query Match             100.0%;  Score 19;  DB 2;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2


RESULT 8
AX463303
LOCUS       AX463303                 25 bp    DNA     linear   PAT 15-JUL-2002
DEFINITION  Sequence 3 from Patent WO0248404.
ACCESSION   AX463303
VERSION     AX463303.1  GI:21886254
KEYWORDS    .
SOURCE      synthetic construct
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  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Becker,M.M.
  TITLE     Method and kit for enhancing the association rates of
            polynucleotides
  JOURNAL   Patent: WO 0248404-A 3 20-JUN-2002;
            Gen-Probe Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 19;  DB 2;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
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Db          6 TGCGGGACTTAACCCAACA 24


RESULT 9
AR112109
LOCUS       AR112109                  26 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 1 from patent US 6130038.
ACCESSION   AR112109
VERSION     AR112109.1  GI:14092009
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Becker,M.M., Majlessi,M. and Brentano,S.T.
  TITLE     Method for amplifying target nucleic acids using modified primers
  JOURNAL   Patent: US 6130038-A 1 10-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .26
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ORIGIN

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Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 10
AR112110/c
LOCUS       AR112110                  26 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 2 from patent US 6130038.
ACCESSION   AR112110
VERSION     AR112110.1  GI:14092010
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Becker,M.M., Majlessi,M. and Brentano,S.T.
  TITLE     Method for amplifying target nucleic acids using modified primers
  JOURNAL   Patent: US 6130038-A 2 10-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .26
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ORIGIN

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Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
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RESULT 11
I93509
LOCUS       I93509                    26 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 5 from patent US 5731148.
ACCESSION   I93509
VERSION     I93509.1  GI:3937979
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Becker,M. and Nelson,N.C.
  TITLE     Adduct protection assay
  JOURNAL   Patent: US 5731148-A 5 24-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .26
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ORIGIN

  Query Match             100.0%;  Score 19;  DB 2;  Length 26;
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Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 12
I93510/c
LOCUS       I93510                    26 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 6 from patent US 5731148.
ACCESSION   I93510
VERSION     I93510.1  GI:3937980
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Becker,M. and Nelson,N.C.
  TITLE     Adduct protection assay
  JOURNAL   Patent: US 5731148-A 6 24-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
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ORIGIN

  Query Match             100.0%;  Score 19;  DB 2;  Length 26;
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Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2


RESULT 13
I93515
LOCUS       I93515                    26 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 11 from patent US 5731148.
ACCESSION   I93515
VERSION     I93515.1  GI:3937985
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Becker,M. and Nelson,N.C.
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  TITLE     Adduct protection assay
  JOURNAL   Patent: US 5731148-A 11 24-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 14
I93516/c
LOCUS       I93516                    26 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 12 from patent US 5731148.
ACCESSION   I93516
VERSION     I93516.1  GI:3937986
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Becker,M. and Nelson,N.C.
  TITLE     Adduct protection assay
  JOURNAL   Patent: US 5731148-A 12 24-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 19;  DB 2;  Length 26;
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2


RESULT 15
AR678434
LOCUS       AR678434                  26 bp    DNA     linear   PAT 13-JUN-2005
DEFINITION  Sequence 4 from patent US 6902891.
ACCESSION   AR678434
VERSION     AR678434.1  GI:67619142
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Laayoun,A., Menou,L., Tora,C., Banerjee,A.R., Becker,M.M.,
            Browne,K.A., Friedenberg,M.C. and Hajjar,F.F.
  TITLE     Process for labeling a nucleic acid
  JOURNAL   Patent: US 6902891-A 4 07-JUN-2005;
            Bio Merieux and Gen-Probe Incorporated; Marcy l' Etoile;
            FRX;
FEATURES             Location/Qualifiers
     source          1. .26
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                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 19;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25
```

```
RESULT 16
AR678435
LOCUS       AR678435                 26 bp    DNA     linear   PAT 13-JUN-2005
DEFINITION  Sequence 5 from patent US 6902891.
ACCESSION   AR678435
VERSION     AR678435.1  GI:67619143
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Laayoun,A., Menou,L., Tora,C., Banerjee,A.R., Becker,M.M.,
            Browne,K.A., Friedenberg,M.C. and Hajjar,F.F.
  TITLE     Process for labeling a nucleic acid
  JOURNAL   Patent: US 6902891-A 5 07-JUN-2005;
            Bio Merieux and Gen-Probe Incorporated; Marcy l' Etoile;
            FRX;
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 17
AR678436
LOCUS       AR678436                 26 bp    DNA     linear   PAT 13-JUN-2005
DEFINITION  Sequence 6 from patent US 6902891.
ACCESSION   AR678436
VERSION     AR678436.1  GI:67619144
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Laayoun,A., Menou,L., Tora,C., Banerjee,A.R., Becker,M.M.,
            Browne,K.A., Friedenberg,M.C. and Hajjar,F.F.
  TITLE     Process for labeling a nucleic acid
  JOURNAL   Patent: US 6902891-A 6 07-JUN-2005;
            Bio Merieux and Gen-Probe Incorporated; Marcy l' Etoile;
            FRX;
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
ORIGIN

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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
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Db          7 TGCGGGACTTAACCCAACA 25


RESULT 18
AR678437
LOCUS       AR678437                 26 bp    RNA     linear   PAT 13-JUN-2005
DEFINITION  Sequence 7 from patent US 6902891.
ACCESSION   AR678437
VERSION     AR678437.1  GI:67619147
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 26)
  AUTHORS   Laayoun,A., Menou,L., Tora,C., Banerjee,A.R., Becker,M.M.,
            Browne,K.A., Friedenberg,M.C. and Hajjar,F.F.
  TITLE     Process for labeling a nucleic acid
  JOURNAL   Patent: US 6902891-A 7 07-JUN-2005;
            Bio Merieux and Gen-Probe Incorporated; Marcy l' Etoile;
            FRX;
FEATURES             Location/Qualifiers
     source          1. .26
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                     /mol_type="unassigned RNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 7.2e+05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 19
AR678438
LOCUS       AR678438                  26 bp    RNA     linear   PAT 13-JUN-2005
DEFINITION  Sequence 8 from patent US 6902891.
ACCESSION   AR678438
VERSION     AR678438.1  GI:67619148
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Laayoun,A., Menou,L., Tora,C., Banerjee,A.R., Becker,M.M.,
            Browne,K.A., Friedenberg,M.C. and Hajjar,F.F.
  TITLE     Process for labeling a nucleic acid
  JOURNAL   Patent: US 6902891-A 8 07-JUN-2005;
            Bio Merieux and Gen-Probe Incorporated; Marcy l' Etoile;
            FRX;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
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ORIGIN

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Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 20
AR678439
LOCUS       AR678439                  26 bp    RNA     linear   PAT 13-JUN-2005
DEFINITION  Sequence 9 from patent US 6902891.
ACCESSION   AR678439
VERSION     AR678439.1  GI:67619149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Laayoun,A., Menou,L., Tora,C., Banerjee,A.R., Becker,M.M.,
            Browne,K.A., Friedenberg,M.C. and Hajjar,F.F.
  TITLE     Process for labeling a nucleic acid
  JOURNAL   Patent: US 6902891-A 9 07-JUN-2005;
            Bio Merieux and Gen-Probe Incorporated; Marcy l' Etoile;
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ORIGIN
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  Query Match             100.0%;  Score 19;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


Search completed: July 26, 2006, 18:08:14
Job time : 1247.2 secs
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SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10743384 and Search Result us-10-743-384-1.szlm60.rng.

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start

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                    GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:         July 26, 2006, 15:45:05 ; Search time 246.293 Seconds
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Scoring table:  IDENTITY_NUC
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Searched:       5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      5397982

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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     Pred. No. is the number of results predicted by chance to have a
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                                    SUMMARIES

                 %
Result           Query
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     1      22  100.0     22  6  ABS71588                Abs71588 Bacterial
     2      22  100.0     22  6  ABS71584                Abs71584 Forward p
```

	3	22	100.0	22	12	ADO15325	Ado15325 PCR prime
	4	22	100.0	52	3	AAA14443	Aaa14443 Escherich
	5	22	100.0	52	5	AAC63206	Aac63206 16S rRNA
c	6	22	100.0	52	5	AAC63204	Aac63204 Capture p
c	7	21	95.5	22	2	AAX60967	Aax60967 Donor pro
	8	20.2	91.8	22	12	ADO15329	Ado15329 PCR prime
c	9	20	90.9	24	10	ABZ23211	Abz23211 PCR prime
	10	18.8	85.5	20	2	AAV51392	Aav51392 Microbial
	11	18	81.8	21	13	ADS15239	Ads15239 H.pylori
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	13	17.8	80.9	30	14	AED50849	Aed50849 16S rRNA
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c	17	17.2	78.2	42	1	AAN92213	Aan92213 Helper ol
c	18	17.2	78.2	42	1	AAN92920	Aan92920 Helper ol
c	19	17.2	78.2	42	5	AAF23125	Aaf23125 N. gonorr
	20	17.2	78.2	46	2	AAQ85201	Aaq85201 Ureaplasm
	21	17.2	78.2	46	2	AAQ85200	Aaq85200 Ureaplasm
c	22	17.2	78.2	46	2	AAQ85163	Aaq85163 Ureaplasm
c	23	17.2	78.2	46	2	AAQ85199	Aaq85199 Ureaplasm
c	24	17	77.3	19	12	ADO18316	Ado18316 Analytica
c	25	17	77.3	19	12	ADO18550	Ado18550 Analytica
c	26	17	77.3	19	12	ADO18518	Ado18518 Analytica
c	27	17	77.3	19	12	ADO18336	Ado18336 Analytica
c	28	16.2	73.6	24	1	AAN90467	Aan90467 Escherich
c	29	16.2	73.6	24	2	AAQ10475	Aaq10475 Probe UP2
c	30	16	72.7	16	2	AAT10133	Aat10133 Primer SA
	31	16	72.7	21	13	ADU74086	Adu74086 Bacillus
c	32	16	72.7	40	2	AAT10136	Aat10136 Modified
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	34	15.6	70.9	57	12	ADO85479	Ado85479 Fungal 18
c	35	15.4	70.0	19	12	ADO18736	Ado18736 Analytica
c	36	15.4	70.0	19	12	ADO18473	Ado18473 Analytica
	37	15.4	70.0	40	3	AAC64803	Aac64803 Novel str
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	43	15	68.2	24	3	AAA14444	Aaa14444 Tether ol
	44	15	68.2	24	5	AAC63205	Aac63205 Fluoresce
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c	46	14.8	67.3	31	3	AAA29977	Aaa29977 PCR prime
c	47	14.8	67.3	50	6	ABZ05357	Abz05357 Human leu
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c	49	14.6	66.4	47	10	ADF16934	Adf16934 Human alb
c	50	14.6	66.4	47	10	ADH22002	Adh22002 Human PYY
c	51	14.4	65.5	18	14	AEC09679	Aec09679 Primer 16
	52	14.4	65.5	50	6	ABZ03588	Abz03588 Human leu
c	53	14.2	64.5	21	14	ACL41182	Acl41182 C20orf103
c	54	14.2	64.5	21	14	ACL41183	Acl41183 C20orf103
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c	56	14.2	64.5	23	14	AEB16517	Aeb16517 Human SLC
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c	58	14.2	64.5	30	14	ADZ71240	Adz71240 Human pla
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ALIGNMENTS

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RESULT 1
ABS71588
ID   ABS71588 standard; DNA; 22 BP.
XX
AC   ABS71588;
XX
DT   28-NOV-2002  (first entry)
XX
DE   Bacterial 16s RNA fragment for primer design #1.
XX
KW   Eubacteria; species detection; speciation; 16s RNA; ds.
XX
OS   Staphylococcus aureus.
```

XX
PN WO200270728-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-US006050.
XX
PR 01-MAR-2001; 2001US-0272642P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Rothman RE, Yang S, Lin S, Kelen GD;
XX
DR WPI; 2002-698755/75.
XX
PT Detecting and determining species source of eubacterial DNA in a sample,
PT comprises amplifying template DNA in the sample using a real-time
PT polymerase chain reaction with the use of primers and at least two
PT fluorogenic probes.
XX
PS Disclosure; Fig 5; 39pp; English.
XX
CC The invention describes a method of detecting and determining species
CC source of eubacterial DNA in a sample. The method comprises amplifying
CC template DNA in the sample using a real-time polymerase chain reaction (R
CC -T PCR), where the PCR or PCR reaction mixture comprises primers and at
CC least two fluorogenic probes. The methods are useful in detecting and
CC determining species source of eubacterial DNA in a sample. The present
CC method allows for highly sensitive detection of any eubacterial species
CC with simultaneous speciation. It eliminates false positive results in
CC detecting bacterial infections. This sequence represents a bacterial 16s
CC RNA sequence used to create primers for use in the eubacterial detection
CC method of the invention
XX
SQ Sequence 22 BP; 5 A; 2 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGAGCATGTGGTTTAATTCGA 22
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Db 1 TGGAGCATGTGGTTTAATTCGA 22

RESULT 2
ABS71584
ID ABS71584 standard; DNA; 22 BP.
XX
AC ABS71584;
XX
DT 28-NOV-2002 (first entry)
XX
DE Forward primer for detecting bacterial infection P890F.
XX
KW Eubacteria; species detection; speciation; 16s RNA; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200270728-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-US006050.
XX
PR 01-MAR-2001; 2001US-0272642P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Rothman RE, Yang S, Lin S, Kelen GD;
XX
DR WPI; 2002-698755/75.
XX
PT Detecting and determining species source of eubacterial DNA in a sample,
PT comprises amplifying template DNA in the sample using a real-time
PT polymerase chain reaction with the use of primers and at least two

```
PT   fluorogenic probes.
XX
PS   Claim 12; Page 11; 39pp; English.
XX
CC   The invention describes a method of detecting and determining species
CC   source of eubacterial DNA in a sample. The method comprises amplifying
CC   template DNA in the sample using a real-time polymerase chain reaction (R
CC   -T PCR), where the PCR or PCR reaction mixture comprises primers and at
CC   least two fluorogenic probes. The methods are useful in detecting and
CC   determining species source of eubacterial DNA in a sample. The present
CC   method allows for highly sensitive detection of any eubacterial species
CC   with simultaneous speciation. It eliminates false positive results in
CC   detecting bacterial infections. This sequence represents a primer
CC   designed using 16s RNA sequences and used in the eubacterial detection
CC   method of the invention
XX
SQ   Sequence 22 BP; 5 A; 2 C; 7 G; 8 T; 0 U; 0 Other;

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  Best Local Similarity   100.0%;  Pred. No. 0.93;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGAGCATGTGGTTTAATTCGA 22
              ||||||||||||||||||||||
Db          1 TGGAGCATGTGGTTTAATTCGA 22


RESULT 3
ADO15325
ID   ADO15325 standard; DNA; 22 BP.
XX
AC   ADO15325;
XX
DT   12-AUG-2004  (first entry)
XX
DE   PCR primer used for one-step real-time RT-PCR detection SeqID 1.
XX
KW   one step real-time RT-PCR; pharmaceutical; cosmetic; bacteria;
KW   fungus-yeast; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2004044247-A2.
XX
PD   27-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-IB005312.
XX
PR   12-NOV-2002; 2002US-0425327P.
XX
PA   (GENO-) GENOLIFE.
XX
PI   Chaubron F,  Martin-Minvielle AC,  Groulon S;
XX
DR   WPI; 2004-411742/38.
XX
PT   Determining presence of bacteria or fungus-yeast RNA in sample involves
PT   carrying out reverse transcriptase-PCR reaction of fungus-yeast RNA and
PT   treating amplified DNA with probes which hybridize to amplified DNA.
XX
PS   Claim 1; SEQ ID NO 1; 31pp; English.
XX
CC   This invention relates to a novel method for one step real-time RT-PCR
CC   kits useful for the detection of microorganisms occurring within
CC   industrial products such as pharmaceuticals, cosmetic and non-clinical
CC   samples. Specifically, it refers to determining the presence of bacteria
CC   or fungus-yeast RNA in a sample suspected of containing such
CC   contaminants. The present invention describes oligonucleotide primers and
CC   probes that are natural nucleic acid or peptide nucleic acid (PNA)
CC   molecules that can hybridise to the target nucleic acid (DNA and RNA).
CC   Accordingly, the method enables rapid and simultaneous detection and
CC   quantification of RNA from bacteria and fungus-yeast in either sterile or
CC   non-sterile products in less than 24 hours. Furthermore, the one step
CC   process reduces the risk of environmental contamination that could occur
CC   when the reaction tubes are opened during the PCR procedure. This
CC   oligonucleotide sequence is a PCR primer used in one-step real time RT-
```

CC PCR to amplify bacteria and fungus-yeast RNA, given in an exemplification
CC of the invention.
XX
SQ Sequence 22 BP; 5 A; 2 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TGGAGCATGTGGTTTAATTCGA 22
              ||||||||||||||||||||||
Db          1 TGGAGCATGTGGTTTAATTCGA 22
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RESULT 4
AAA14443
ID AAA14443 standard; DNA; 52 BP.
XX
AC AAA14443;
XX
DT 21-AUG-2000 (first entry)
XX
DE Escherichia coli 16S rRNA gene fragment template.
XX
KW Reverse displacement assay; nucleic acid detection; hybridisation;
KW 16S ribosomal RNA gene; ss.
XX
OS Escherichia coli.
XX
PN WO200020643-A1.
XX
PD 13-APR-2000.
XX
PF 04-OCT-1999; 99WO-US023035.
XX
PR 05-OCT-1998; 98US-0103075P.
XX
PA (MOSA-) MOSAIC TECHNOLOGIES.
XX
PI Abrams ES, Hammond PW;
XX
DR WPI; 2000-303807/26.
XX
PT Method for detecting the presence of a target nucleic acid sequence in a
PT test sample.
XX
PS Example; Page 17; 30pp; English.
XX
CC The invention relates to a novel method for detecting the presence of a
CC target nucleic acid sequence in a test sample. The method comprises
CC forming a probe-tether complex and introducing a test sample into a
CC solution containing the complex under conditions suitable for
CC hybridisation between the probe and the target. A probe-target complex is
CC formed, and the presence of the target nucleic acid sequence is detected
CC in the test sample. The probe is complementary to the target sequence,
CC while the tether is complementary to at least one subsequence of the
CC probe. The probe-complex is contains at least one double stranded segment
CC and one single stranded segment. Introduction of the target nucleic acid
CC sequence displaces the tether sequence from the probe. If the probe
CC and/or the tether contain a detectable label (e.g., a fluorophore), the
CC reverse displacement can be detected by an alteration in the signal
CC produced. Saturation of the tether nucleic acid with labelled probe is
CC not required in this method, unlike prior art methods. Because the tether
CC nucleic acid is not complementary to the target nucleic acid, uncomplexed
CC tether nucleic acid will not hybridise with the target, and therefore
CC does not compete with target nucleic acid for hybridisation with probe
CC nucleic acids. In the exemplification of the invention, an
CC oligonucleotide (AAA14443) corresponding to a portion of the Escherichia
CC coli 16S ribosomal RNA gene was detected according to the method of the
CC invention using probe AAA14445 and tether oligonucleotide AAA14444. The
CC present sequence represents the Escherichia coli 16S ribosomal RNA gene
CC fragment used as the target nucleic acid
XX
SQ Sequence 52 BP; 15 A; 12 C; 14 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 3; Length 52;

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  Best Local Similarity   100.0%;  Pred. No. 1;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGAGCATGTGGTTTAATTCGA 22
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Db         10 TGGAGCATGTGGTTTAATTCGA 31


RESULT 5
AAC63206
ID   AAC63206 standard; DNA; 52 BP.
XX
AC   AAC63206;
XX
DT   06-FEB-2001  (first entry)
XX
DE   16S rRNA fragment.
XX
KW   Microorganism detection; 16S rRNA; ss.
XX
OS   Escherichia coli.
XX
PN   WO200060120-A2.
XX
PD   12-OCT-2000.
XX
PF   31-MAR-2000; 2000WO-US008773.
XX
PR   02-APR-1999;   99US-00286091.
XX
PA   (MOSA-) MOSAIC TECHNOLOGIES.
XX
PI   Boles TC;
XX
DR   WPI; 2001-015657/02.
XX
PT   Detecting presence or absence of microbial target molecules
PT   electrophoretically, by using capture probes immobilized to
PT   electrophoretic matrix, that specifically bind to target molecule in test
PT   sample.
XX
PS   Claim 27; Page 35; 61pp; English.
XX
CC   The present invention relates to a method for detecting the presence or
CC   absence of a microorganism in a biological sample by electrophoresis. The
CC   method of the present invention comprises detecting the presence or
CC   absence of microbiological target molecules in a test sample using
CC   capture probes, immobilised to an electrophoretic medium, which
CC   specifically bind to or are bound by the specific microbiological target
CC   molecules. The method of the present invention is useful for identifying
CC   bacteria Serratia marcescens, Staphylococcus epidermidis, Staphylococcus
CC   aureus, Escherichia coli, Bacillus cereus, Enterobacter cloacae,
CC   Streptococcus pyogenes, Staphylococcus warneri, Streptococcus (alpha-
CC   hemolytic), Streptococcus mitis, Salmonella, Serratia liquifaciens,
CC   Klebsiella, Propionibacterium acnes, Yersinia enterocolitica, Pseudomonas
CC   fluorescens, Pseudomonas putida in a biological sample. The present
CC   sequence is a DNA corresponding to the 16S rRNA sequence of E. coli. This
CC   sequence was used as a microbiological target molecule in the method of
CC   the present invention
XX
SQ   Sequence 52 BP; 15 A; 12 C; 14 G; 11 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 22;  DB 5;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 1;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGAGCATGTGGTTTAATTCGA 22
              ||||||||||||||||||||||
Db         10 TGGAGCATGTGGTTTAATTCGA 31


RESULT 6
AAC63204/c
ID   AAC63204 standard; DNA; 52 BP.
XX
AC   AAC63204;
```

XX
DT 06-FEB-2001 (first entry)
XX
DE Capture probe #2 used for detecting microorganisms.
XX
KW Microorganism detection; capture probe; ss.
XX
OS Escherichia coli.
XX
PN WO200060120-A2.
XX
PD 12-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US008773.
XX
PR 02-APR-1999; 99US-00286091.
XX
PA (MOSA-) MOSAIC TECHNOLOGIES.
XX
PI Boles TC;
XX
DR WPI; 2001-015657/02.
XX
PT Detecting presence or absence of microbial target molecules
PT electrophoretically, by using capture probes immobilized to
PT electrophoretic matrix, that specifically bind to target molecule in test
PT sample.
XX
PS Claim 25; Page 34; 61pp; English.
XX
CC The present invention relates to a method for detecting the presence or
CC absence of a microorganism in a biological sample by electrophoresis. The
CC method of the present invention comprises detecting the presence or
CC absence of microbiological target molecules in a test sample using
CC capture probes, immobilised to an electrophoretic medium, which
CC specifically bind to or are bound by the specific microbiological target
CC molecules. The method of the present invention is useful for identifying
CC bacteria Serratia marcescens, Staphylococcus epidermidis, Staphylococcus
CC aureus, Escherichia coli, Bacillus cereus, Enterobacter cloacae,
CC Streptococcus pyogenes, Staphylococcus warneri, Streptococcus (alpha-
CC hemolytic), Streptococcus mitis, Salmonella, Serratia liquifaciens,
CC Klebsiella, Propionibacterium acnes, Yersinia enterocolitica, Pseudomonas
CC fluorescens, Pseudomonas putida in a biological sample. The present
CC sequence is a capture probe used in the method of the present invention
XX
SQ Sequence 52 BP; 11 A; 14 C; 12 G; 15 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 5; Length 52;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TGGAGCATGTGGTTTAATTCGA 22
              ||||||||||||||||||||||
Db         43 TGGAGCATGTGGTTTAATTCGA 22
```

RESULT 7
AAX60967/c
ID AAX60967 standard; DNA; 22 BP.
XX
AC AAX60967;
XX
DT 03-SEP-1999 (first entry)
XX
DE Donor probe hybridising to a conserved eubacterial 16S rRNA.
XX
KW Nucleic acid detection; target; protein detection; pathogenic microbe;
KW eubacteria; human immune deficiency virus; blood contamination;
KW hybridisation; probe; ss.
XX
OS Synthetic.
XX
PN WO9926724-A2.
XX
PD 03-JUN-1999.
XX

```
PF   25-NOV-1998;   98WO-US024918.
XX
PR   25-NOV-1997;   97US-0066508P.
XX
PA   (MOSA-) MOSAIC TECHNOLOGIES.
XX
PI   Muir AR,  Boles TC,  Adams CP;
XX
DR   WPI; 1999-385182/32.
XX
PT   Device for detecting target molecule or microbe.
XX
PS   Example 11; Page 78; 124pp; English.
XX
CC   The invention describes a device for detecting presence of a target
CC   molecule in a biological sample. The device comprises a receptacle
CC   housing at least one chamber, having at least one compartment containing
CC   one or more reagents for detecting the target. Optionally the device is
CC   combined with, and optionally removable from, a collection device. The
CC   devices are used to detect specific nucleic acids (RNA or DNA), proteins,
CC   polypeptides, or a very wide range of pathogenic microbes (bacteria,
CC   viruses, fungi or parasites), particularly eubacteria or human immune
CC   deficiency virus. Especially the method is used to detect contamination
CC   of donated blood. The devices are efficient, easy to use and provide
CC   results rapidly
XX
SQ   Sequence 22 BP; 8 A; 8 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             95.5%;  Score 21;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGAGCATGTGGTTTAATTCG 21
              |||||||||||||||||||||
Db         21 TGGAGCATGTGGTTTAATTCG 1


RESULT 8
ADO15329
ID   ADO15329 standard; DNA; 22 BP.
XX
AC   ADO15329;
XX
DT   12-AUG-2004  (first entry)
XX
DE   PCR primer used for one-step real-time RT-PCR detection SeqID 5.
XX
KW   one step real-time RT-PCR; pharmaceutical; cosmetic; bacteria;
KW   fungus-yeast; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2004044247-A2.
XX
PD   27-MAY-2004.
XX
PF   03-NOV-2003; 2003WO-IB005312.
XX
PR   12-NOV-2002; 2002US-0425327P.
XX
PA   (GENO-) GENOLIFE.
XX
PI   Chaubron F,  Martin-Minvielle AC,  Groulon S;
XX
DR   WPI; 2004-411742/38.
XX
PT   Determining presence of bacteria or fungus-yeast RNA in sample involves
PT   carrying out reverse transcriptase-PCR reaction of fungus-yeast RNA and
PT   treating amplified DNA with probes which hybridize to amplified DNA.
XX
PS   Claim 1; SEQ ID NO 5; 31pp; English.
XX
CC   This invention relates to a novel method for one step real-time RT-PCR
CC   kits useful for the detection of microorganisms occurring within
CC   industrial products such as pharmaceuticals, cosmetic and non-clinical
CC   samples. Specifically, it refers to determining the presence of bacteria
```

```
RESULT 3
US-09-411-777A-1
; Sequence 1, Application US/09411777A
; Patent No. 6238927
; GENERAL INFORMATION:
;  APPLICANT:  Abrams, Ezra S.
;  APPLICANT:  Hammond, Philip W.
;  TITLE OF INVENTION:  Reverse Displacement Assay for Detection
;  TITLE OF INVENTION:  of Nucleic Acid Sequences
;  FILE REFERENCE:  MST98-03pA
;  CURRENT APPLICATION NUMBER: US/09/411,777A
;  CURRENT FILING DATE:  1999-10-04
;  PRIOR APPLICATION NUMBER:  60/103,075
;  PRIOR FILING DATE:  1998-10-05
;  NUMBER OF SEQ ID NOS:  3
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 52
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: target oligonucleotide
US-09-411-777A-1

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Qy          1 TGGAGCATGTGGTTTAATTCGA 22
              ||||||||||||||||||||||
Db         10 TGGAGCATGTGGTTTAATTCGA 31
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SCORE Search Results Details for Application 10743384 and Search Result us-10-743-384-1.szlm60.rge..

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OM nucleic - nucleic search, using sw model

Run on:         July 26, 2006, 15:49:16 ; Search time 1441.8 Seconds
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Perfect score:  22
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      2455354

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Maximum DB seq length: 60

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

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     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                    SUMMARIES

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Result            Query
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     2       22  100.0     22  2  AR478753                AR478753 Sequence
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	3	22	100.0	22	2	AR478757	AR478757 Sequence
	4	22	100.0	52	2	AR154667	AR154667 Sequence
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	6	20.4	92.7	22	2	AR478761	AR478761 Sequence
	7	20.2	91.8	22	2	CQ818168	CQ818168 Sequence
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	9	20	90.9	25	2	AR089512	AR089512 Sequence
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c	37	14.2	64.5	51	2	CQ002165	CQ002165 Sequence
	38	14.2	64.5	60	2	CQ537315	CQ537315 Sequence
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c	40	13.6	61.8	21	2	AR299176	AR299176 Sequence
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ALIGNMENTS

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CQ818164
LOCUS       CQ818164                  22 bp    DNA     linear   PAT 07-JUN-2004
DEFINITION  Sequence 1 from Patent WO2004044247.
ACCESSION   CQ818164
VERSION     CQ818164.1  GI:48426956
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Chaubron,F., Martin-Minvielle,A.C. and Groulon,S.
  TITLE     One step real-time rt pcr kits for the universal detection of
```

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            organisms in industrial products
  JOURNAL   Patent: WO 2004044247-A 1 27-MAY-2004;
            Genolife (FR)
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="#Description of artificial sequence:
                      oligonucleotide primer#"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGAGCATGTGGTTTAATTCGA 22
              ||||||||||||||||||||||
Db          1 TGGAGCATGTGGTTTAATTCGA 22


RESULT 2
AR478753
LOCUS       AR478753                  22 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 1 from patent US 6699670.
ACCESSION   AR478753
VERSION     AR478753.1  GI:47237473
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Rothman,R.E., Yang,S., Lin,S. and Kelen,G.D.
  TITLE     Quantitative assay for the simultaneous detection and speciation of
            bacterial infections
  JOURNAL   Patent: US 6699670-A 1 02-MAR-2004;
            The Johns Hopkins University; Baltimore, MD
FEATURES              Location/Qualifiers
     source           1. .22
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 4.1e+05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGAGCATGTGGTTTAATTCGA 22
              ||||||||||||||||||||||
Db          1 TGGAGCATGTGGTTTAATTCGA 22


RESULT 3
AR478757
LOCUS       AR478757                  22 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 5 from patent US 6699670.
ACCESSION   AR478757
VERSION     AR478757.1  GI:47237477
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Rothman,R.E., Yang,S., Lin,S. and Kelen,G.D.
  TITLE     Quantitative assay for the simultaneous detection and speciation of
            bacterial infections
  JOURNAL   Patent: US 6699670-A 5 02-MAR-2004;
            The Johns Hopkins University; Baltimore, MD
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+05;
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  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGAGCATGTGGTTTAATTCGA 22
              ||||||||||||||||||||||
Db          1 TGGAGCATGTGGTTTAATTCGA 22


RESULT 4
AR154667
LOCUS       AR154667                  52 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6238927.
ACCESSION   AR154667
VERSION     AR154667.1  GI:15122720
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Abrams,E.S. and Hammond,P.W.
  TITLE     Reverse displacement assay for detection of nucleic acid sequences
  JOURNAL   Patent: US 6238927-A 1 29-MAY-2001;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 2;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+05;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGAGCATGTGGTTTAATTCGA 22
              ||||||||||||||||||||||
Db         10 TGGAGCATGTGGTTTAATTCGA 31


RESULT 5
AR159998/c
LOCUS       AR159998                  22 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 2 from patent US 6251660.
ACCESSION   AR159998
VERSION     AR159998.1  GI:16222896
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Muir,A.R., Boles,T.Christian. and Adams,C.P.
  TITLE     Devices and methods for detecting target molecules in biological
            samples
  JOURNAL   Patent: US 6251660-A 2 26-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             95.5%;  Score 21;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+05;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGAGCATGTGGTTTAATTCG 21
              |||||||||||||||||||||
Db         21 TGGAGCATGTGGTTTAATTCG 1


RESULT 6
AR478761
LOCUS       AR478761                  22 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 9 from patent US 6699670.
ACCESSION   AR478761
VERSION     AR478761.1  GI:47237481
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Rothman,R.E., Yang,S., Lin,S. and Kelen,G.D.
  TITLE     Quantitative assay for the simultaneous detection and speciation of
            bacterial infections
  JOURNAL   Patent: US 6699670-A 9 02-MAR-2004;
            The Johns Hopkins University; Baltimore, MD
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             92.7%;  Score 20.4;  DB 2;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 8e+05;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGGAGCATGTGGTTTAATTCGA 22
              ||||||||| ||||||||||||
Db          1 TGGAGCATGCGGTTTAATTCGA 22


RESULT 7
CQ818168
LOCUS       CQ818168                  22 bp    DNA     linear   PAT 07-JUN-2004
DEFINITION  Sequence 5 from Patent WO2004044247.
ACCESSION   CQ818168
VERSION     CQ818168.1  GI:48426960
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Chaubron,F., Martin-Minvielle,A.C. and Groulon,S.
  TITLE     One step real-time rt pcr kits for the universal detection of
            organisms in industrial products
  JOURNAL   Patent: WO 2004044247-A 5 27-MAY-2004;
            Genolife (FR)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="#Description of artificial sequence:
                     oligonucleotide primer#"
ORIGIN

  Query Match             91.8%;  Score 20.2;  DB 2;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 8.7e+05;
  Matches   19;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGAGCATGTGGTTTAATTCG 21
              :|||||||||||:||||||||
Db          2 YGGAGCATGTGGYTTAATTCG 22


RESULT 8
AX622955/c
LOCUS       AX622955                  24 bp    DNA     linear   PAT 20-FEB-2003
DEFINITION  Sequence 17 from Patent WO02095413.
ACCESSION   AX622955
VERSION     AX622955.1  GI:28450896
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Brunham,R.C., Karunakaran,P. and Blanchard,J.
  TITLE     Diagnosis of vascular disease susceptibility using bacteriophage
            phi-cpn1 host chlamydia
  JOURNAL   Patent: WO 02095413-A 17 28-NOV-2002;
            UNIVERSITY OF BRITISH COLUMBIA (CA)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
```

```
                    /note="oligonucleotide primer for the 16s gene: reverse"
ORIGIN

  Query Match             90.9%;  Score 20;  DB 2;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGAGCATGTGGTTTAATTC 20
              ||||||||||||||||||||
Db         20 TGGAGCATGTGGTTTAATTC 1


RESULT 9
AR089512
LOCUS       AR089512                  25 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 271 from patent US 5994066.
ACCESSION   AR089512
VERSION     AR089512.1  GI:10016269
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.
  TITLE     Species-specific and universal DNA probes and amplification primers
            to rapidly detect and identify common bacterial pathogens and
            associated antibiotic resistance genes from clinical specimens for
            routine diagnosis in microbiology laboratories
  JOURNAL   Patent: US 5994066-A 271 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             90.9%;  Score 20;  DB 2;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGAGCATGTGGTTTAATTC 20
              ||||||||||||||||||||
Db          6 TGGAGCATGTGGTTTAATTC 25


RESULT 10
CS246054/c
LOCUS       CS246054                  30 bp    DNA     linear   PAT 09-JAN-2006
DEFINITION  Sequence 101 from Patent EP1609874.
ACCESSION   CS246054
VERSION     CS246054.1  GI:84660518
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Perseu,S.
  TITLE     System for searching for and identifying pathogenic agents
  JOURNAL   Patent: EP 1609874-A 101 28-DEC-2005;
            Bioanalisi Centro Sud S.n.c. di Perseu Sinibaldo eC. (IT)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probe"
ORIGIN

  Query Match             90.9%;  Score 20;  DB 2;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 9e+05;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGAGCATGTGGTTTAATTC 20
              ||||||||||||||||||||
Db         20 TGGAGCATGTGGTTTAATTC 1
```

SCORE Search Results Details for Application 10743384 and Search Result us-10-743-384-2.szlm60.rng.

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OM nucleic - nucleic search, using sw model

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                                          (without alignments)
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Title:          US-10-743-384-2
Perfect score:  19
Sequence:       1 tgcgggacttaacccaaca 19

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      5397982

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Database :       N_Geneseq_8:*
                1:  geneseqn1980s:*
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     Pred. No. is the number of results predicted by chance to have a
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                                    SUMMARIES

                    %
Result              Query
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-------------------------------------------------------------------------------
     1       19    100.0      19   6  ABS71585                Abs71585 Reverse p
c    2       19    100.0      19   6  ABS71591                Abs71591 Bacterial
```

	3	19	100.0	19	12	ADO15326	Ado15326 PCR prime
	4	19	100.0	20	8	ACC48547	Acc48547 Affinity-
	5	19	100.0	21	2	AAT45274	Aat45274 Bacterial
	6	19	100.0	21	5	AAS11044	Aas11044 Bacterial
c	7	19	100.0	23	1	AAN82163	Aan82163 Sequence
c	8	19	100.0	23	2	AAV45647	Aav45647 Probe for
c	9	19	100.0	23	2	AAV62776	Aav62776 Probe for
c	10	19	100.0	23	3	AAZ44009	Aaz44009 Enterobac
c	11	19	100.0	23	4	AAH44156	Aah44156 Escherich
	12	19	100.0	25	6	ABK90486	Abk90486 Synthetic
c	13	19	100.0	25	12	ADP47355	Adp47355 Intellige
c	14	19	100.0	25	12	ADQ59713	Adq59713 Intellige
c	15	19	100.0	25	14	AED28542	Aed28542 Primer fo
	16	19	100.0	26	1	AAN80834	Aan80834 Probe no.
	17	19	100.0	26	1	AAN97224	Aan97224 Probe con
	18	19	100.0	26	2	AAQ55675	Aaq55675 Amine lin
	19	19	100.0	26	2	AAT73684	Aat73684 RNA acrid
	20	19	100.0	26	2	AAT73680	Aat73680 Acridiniu
	21	19	100.0	26	2	AAT43265	Aat43265 Probe #4
	22	19	100.0	26	2	AAV01611	Aav01611 Linker-mo
c	23	19	100.0	26	2	AAV06803	Aav06803 Target ol
	24	19	100.0	26	2	AAV06802	Aav06802 Modified
	25	19	100.0	26	2	AAT86639	Aat86639 Oligonucl
	26	19	100.0	26	2	AAZ09277	Aaz09277 Acridiniu
	27	19	100.0	26	3	AAZ60216	Aaz60216 Probe #1
	28	19	100.0	26	3	AAZ95615	Aaz95615 Linker re
	29	19	100.0	26	3	AAZ95618	Aaz95618 Linker re
	30	19	100.0	26	4	AAH44126	Aah44126 DNA label
	31	19	100.0	26	4	AAH44125	Aah44125 DNA label
	32	19	100.0	26	4	AAH44128	Aah44128 RNA-alpha
	33	19	100.0	26	4	AAH44129	Aah44129 RNA-alpha
	34	19	100.0	26	4	AAH44127	Aah44127 DNA label
	35	19	100.0	26	4	AAH44130	Aah44130 RNA fragm
	36	19	100.0	26	5	AAF23080	Aaf23080 Campyloba
	37	19	100.0	26	5	AAF23102	Aaf23102 Bacterial
	38	19	100.0	26	6	ABK90484	Abk90484 Synthetic
c	39	19	100.0	26	6	ABK90485	Abk90485 Synthetic
	40	19	100.0	26	6	ABS52480	Abs52480 RNA seque
	41	19	100.0	26	6	ABS52479	Abs52479 DNA seque
	42	19	100.0	26	6	ABS52481	Abs52481 RNA seque
	43	19	100.0	26	6	ABS52482	Abs52482 RNA seque
	44	19	100.0	26	6	ABS52477	Abs52477 DNA seque
	45	19	100.0	26	6	ABS52478	Abs52478 DNA seque
c	46	19	100.0	26	8	ACC48545	Acc48545 Target RN
	47	19	100.0	26	8	ACC48546	Acc48546 Affinity-
c	48	19	100.0	51	12	ADO85475	Ado85475 Bacterial
c	49	19	100.0	59	2	AAV79269	Aav79269 Staphyloc
c	50	18	94.7	19	12	ADP47513	Adp47513 Intellige
c	51	18	94.7	19	12	ADP47583	Adp47583 Intellige
c	52	18	94.7	19	12	ADP47579	Adp47579 Intellige
c	53	18	94.7	19	12	ADP47585	Adp47585 Intellige
c	54	18	94.7	19	12	ADQ59871	Adq59871 Intellige
c	55	18	94.7	19	12	ADQ59943	Adq59943 Intellige
c	56	18	94.7	19	12	ADQ59941	Adq59941 Intellige
c	57	18	94.7	19	12	ADQ59937	Adq59937 Intellige
c	58	18	94.7	19	14	AED28541	Aed28541 Primer fo
c	59	18	94.7	55	8	ACC97177	Acc97177 Consensus
	60	17.4	91.6	26	5	AAF23118	Aaf23118 N. gonorr

ALIGNMENTS

```
RESULT 1
ABS71585
ID   ABS71585 standard; DNA; 19 BP.
XX
AC   ABS71585;
XX
DT   28-NOV-2002  (first entry)
XX
DE   Reverse primer for detecting bacterial infection P1033R.
XX
KW   Eubacteria; species detection; speciation; 16s RNA; PCR; primer; ss.
XX
OS   Synthetic.
```

XX
PN WO200270728-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-US006050.
XX
PR 01-MAR-2001; 2001US-0272642P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Rothman RE, Yang S, Lin S, Kelen GD;
XX
DR WPI; 2002-698755/75.
XX
PT Detecting and determining species source of eubacterial DNA in a sample,
PT comprises amplifying template DNA in the sample using a real-time
PT polymerase chain reaction with the use of primers and at least two
PT fluorogenic probes.
XX
PS Claim 12; Page 11; 39pp; English.
XX
CC The invention describes a method of detecting and determining species
CC source of eubacterial DNA in a sample. The method comprises amplifying
CC template DNA in the sample using a real-time polymerase chain reaction (R
CC -T PCR), where the PCR or PCR reaction mixture comprises primers and at
CC least two fluorogenic probes. The methods are useful in detecting and
CC determining species source of eubacterial DNA in a sample. The present
CC method allows for highly sensitive detection of any eubacterial species
CC with simultaneous speciation. It eliminates false positive results in
CC detecting bacterial infections. This sequence represents a primer
CC designed using 16s RNA sequences and used in the eubacterial detection
CC method of the invention
XX
SQ Sequence 19 BP; 6 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19
||||||||||||||||||||
Db 1 TGCGGGACTTAACCCAACA 19

RESULT 2
ABS71591/c
ID ABS71591 standard; DNA; 19 BP.
XX
AC ABS71591;
XX
DT 28-NOV-2002 (first entry)
XX
DE Bacterial 16s RNA fragment for primer design #4.
XX
KW Eubacteria; species detection; speciation; 16s RNA; ds.
XX
OS Staphylococcus aureus.
XX
PN WO200270728-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-US006050.
XX
PR 01-MAR-2001; 2001US-0272642P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Rothman RE, Yang S, Lin S, Kelen GD;
XX
DR WPI; 2002-698755/75.
XX
PT Detecting and determining species source of eubacterial DNA in a sample,
PT comprises amplifying template DNA in the sample using a real-time
PT polymerase chain reaction with the use of primers and at least two

PT fluorogenic probes.
XX
PS Disclosure; Fig 5; 39pp; English.
XX
CC The invention describes a method of detecting and determining species
CC source of eubacterial DNA in a sample. The method comprises amplifying
CC template DNA in the sample using a real-time polymerase chain reaction (R
CC -T PCR), where the PCR or PCR reaction mixture comprises primers and at
CC least two fluorogenic probes. The methods are useful in detecting and
CC determining species source of eubacterial DNA in a sample. The present
CC method allows for highly sensitive detection of any eubacterial species
CC with simultaneous speciation. It eliminates false positive results in
CC detecting bacterial infections. This sequence represents a bacterial 16s
CC RNA sequence used to create primers for use in the eubacterial detection
CC method of the invention
XX
SQ Sequence 19 BP; 3 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19
||||||||||||||||||||
Db 19 TGCGGGACTTAACCCAACA 1

RESULT 3
ADO15326
ID ADO15326 standard; DNA; 19 BP.
XX
AC ADO15326;
XX
DT 12-AUG-2004 (first entry)
XX
DE PCR primer used for one-step real-time RT-PCR detection SeqID 2.
XX
KW one step real-time RT-PCR; pharmaceutical; cosmetic; bacteria;
KW fungus-yeast; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO2004044247-A2.
XX
PD 27-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-IB005312.
XX
PR 12-NOV-2002; 2002US-0425327P.
XX
PA (GENO-) GENOLIFE.
XX
PI Chaubron F, Martin-Minvielle AC, Groulon S;
XX
DR WPI; 2004-411742/38.
XX
PT Determining presence of bacteria or fungus-yeast RNA in sample involves
PT carrying out reverse transcriptase-PCR reaction of fungus-yeast RNA and
PT treating amplified DNA with probes which hybridize to amplified DNA.
XX
PS Claim 1; SEQ ID NO 2; 31pp; English.
XX
CC This invention relates to a novel method for one step real-time RT-PCR
CC kits useful for the detection of microorganisms occurring within
CC industrial products such as pharmaceuticals, cosmetic and non-clinical
CC samples. Specifically, it refers to determining the presence of bacteria
CC or fungus-yeast RNA in a sample suspected of containing such
CC contaminants. The present invention describes oligonucleotide primers and
CC probes that are natural nucleic acid or peptide nucleic acid (PNA)
CC molecules that can hybridise to the target nucleic acid (DNA and RNA).
CC Accordingly, the method enables rapid and simultaneous detection and
CC quantification of RNA from bacteria and fungus-yeast in either sterile or
CC non-sterile products in less than 24 hours. Furthermore, the one step
CC process reduces the risk of environmental contamination that could occur
CC when the reaction tubes are opened during the PCR procedure. This
CC oligonucleotide sequence is a PCR primer used in one-step real time RT-

```
CC   PCR to amplify bacteria and fungus-yeast RNA, given in an exemplification
CC   of the invention.
XX
SQ   Sequence 19 BP; 6 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 19;  DB 12;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db          1 TGCGGGACTTAACCCAACA 19


RESULT 4
ACC48547
ID   ACC48547 standard; DNA; 20 BP.
XX
AC   ACC48547;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Affinity-labeled probe for nucleic acid detection.
XX
KW   Nucleic acid detection; affinity-shifted probe; ss.
XX
OS   Escherichia coli.
XX
FH   Key             Location/Qualifiers
FT   modified_base   10. .11
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= labelled with acridinium ester"
XX
PN   WO2003020952-A2.
XX
PD   13-MAR-2003.
XX
PF   30-AUG-2002; 2002WO-US027710.
XX
PR   31-AUG-2001; 2001US-0316770P.
PR   26-MAR-2002; 2002US-0368072P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Becker MM,  Nelson NC;
XX
DR   WPI; 2003-313092/30.
XX
PT   Novel probe reagent for quantifying amount of analyte polynucleotide
PT   present in test sample in lower or higher amounts, has two or more probes
PT   that hybridize with same analyte polynucleotide with different
PT   affinities.
XX
PS   Example 1; Page 44; 84pp; English.
XX
CC   The present invention relates to the use of multiple probes for
CC   quantifying analytes over an extended dynamic range. To demonstrate the
CC   basis of the quantitative approach underlying the invention, an
CC   experiment was conducted using 3 types of hybridisation reaction, each
CC   reaction being characterised by its own dynamic range. The present
CC   sequence is that of a second probe used in the procedure. It is a 20-mer
CC   labelled with acridinium ester (AE) to a specific activity of 9.37 x 10
CC   power 7 rlu/pmole. A first 26-mer probe (see ACC48547) was labelled with
CC   AE to a specific activity of 1.31 x 10 power 8 rlu/pmole. The target was
CC   an RNA sequence (see ACC48545) from Escherichia coli. The first set of
CC   hybridisation reactions included 0.5 fmol of the 26-mer probe, the second
CC   set used 0.5 fmol of the 20-mer, and the third used 0.5 fmol of each
CC   probe. The 26-mer and 20-mer probes were separately useful for
CC   quantifying the analyte over 10-1,000 and 1,000-100,000 fmol ranges,
CC   respectively, but together provided a quantitative range from 10 to
CC   100,000 fmol. The results showed how 2 different probes harbouring
CC   indistinguishable labels and binding the same analyte with a different
CC   measurable interaction can be used to quantify the analyte over an
CC   extended dynamic range
XX
```

```
SQ   Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 19;  DB 8;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          1 TGCGGGACTTAACCCAACA 19


RESULT 5
AAT45274
ID   AAT45274 standard; DNA; 21 BP.
XX
AC   AAT45274;
XX
DT   06-AUG-1997  (first entry)
XX
DE   Bacterial 16S rRNA V6 variable region amplification primer.
XX
KW   Ribosomal RNA; 16S rRNA; V6 variable region; diagnostic probe;
KW   species-specific; amplification primer; polymerase chain reaction; PCR;
KW   Clavibacter michiganensis; ss.
XX
OS   Synthetic.
XX
PN   FR2733754-A1.
XX
PD   08-NOV-1996.
XX
PF   05-MAY-1995;   95FR-00005416.
XX
PR   05-MAY-1995;   95FR-00005416.
XX
PA   (UYAN-) UNIV ANGERS.
XX
PI   Horvais A;
XX
DR   WPI; 1997-001737/01.
XX
PT   Clavibacter michiganensis DNA fragments - useful as diagnostic probes and
PT   primers.
XX
PS   Disclosure; Page 20; 29pp; French.
XX
CC   Genomic DNA coding for the V6 variable region of 16S ribosomal RNA was
CC   amplified from 7 different bacterial strains using PCR primers having the
CC   sequences given in AAT45273 and AAT45274. The bacteria were divided into
CC   three groups: the first group contained 2 different sub-species of
CC   Clavibacter michiganensis; the second group contained 2 non-michiganensis
CC   Clavibacter species and the third group consisted of 3 varieties of
CC   Curtobacterium flaccumfaciens. The amplification products were sequenced
CC   and a consensus sequence was derived for each of the three groups. A
CC   comparison of the three consensus sequences allowed a sequence specific
CC   to C.michiganensis V6 variable region to be identified, i.e. the sequence
CC   in AAT45270. Single-stranded fragments which have at least 70% homology
CC   with the identified sequence or their complementary sequences are
CC   claimed. The new DNA fragments are used as probes and primers for
CC   detecting C.michiganensis infections, e.g. in tomatoes
XX
SQ   Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 19;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          2 TGCGGGACTTAACCCAACA 20


RESULT 6
AAS11044
ID   AAS11044 standard; DNA; 21 BP.
XX
```

```
AC   AAS11044;
XX
DT   06-AUG-2003  (revised)
DT   24-OCT-2001  (first entry)
XX
DE   Bacterial 16s RNA antisense oligomer #10.
XX
KW   Antisense; bacterial 16s ribosomal RNA; rRNA; bacterial infection; human;
KW   food grain supplement; livestock; poultry; therapeutic; ss.
XX
OS   Vibrio cholerae.
OS   Escherichia coli.
OS   Salmonella typhimurium.
OS   Shigella dysenteriae.
OS   Haemophilus influenzae.
OS   Pseudomonas aeruginosa.
OS   Neisseria gonorrhoeae.
OS   Staphylococcus aureus.
OS   Mycobacterium tuberculosis.
OS   Helicobacter pylori.
OS   Streptococcus pneumoniae.
OS   Treponema pallidum.
OS   Chlamydia trachomatis.
OS   Bartonella henselae.
XX
PN   WO200142457-A2.
XX
PD   14-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-US042391.
XX
PR   29-NOV-1999;   99US-0168150P.
XX
PA   (AVIB-) AVI BIOPHARMA INC.
XX
PI   Iversen PL;
XX
DR   WPI; 2001-457295/49.
XX
PT   Antibacterial compound, useful for treating bacterial infections and as
PT   livestock and poultry food supplement, comprises antisense
PT   oligonucleotides complementary to bacterial 16S and 23S rRNA.
XX
PS   Claim 11; Page 44; 62pp; English.
XX
CC   AAS11035-AAS11157 represent the coding sequences of bacterial 16S
CC   ribosomal RNA (rRNA) antisense oligomers. These sequences are
CC   antibacterial compounds comprising substantially uncharged antisense
CC   oligomers containing 8-40 nucleotide subunits, including a targeting
CC   nucleic acid sequence at least 10 nucleotides in length which is
CC   complementary to a bacterial 16S or 23S rRNA nucleic acid sequence. The
CC   antisense oligomers are used for treating a bacterial infection in a
CC   human or a mammalian animal produced by Escherichia coli, Salmonella
CC   typhimurium, Pseudomonas aeruginosa, Vibrio cholera, Neisseria
CC   gonorrhoea, Helicobacter pylori, Bartonella henselae, Haemophilus
CC   influenza, Shigella dysenterae, Staphylococcus aureus, Mycobacterium
CC   tuberculosis, Streptococcus pneumoniae, Treponema palladium and Chlamydia
CC   trachomatis. The antibacterial compound may be used as a food grain
CC   supplement in livestock and poultry food composition. (Updated on 06-AUG-
CC   2003 to correct OS field.)
XX
SQ   Sequence 21 BP; 6 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 19;  DB 5;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          2 TGCGGGACTTAACCCAACA 20


RESULT 7
AAN82163/c
ID   AAN82163 standard; DNA; 23 BP.
XX
```

```
AC   AAN82163;
XX
DT   25-MAR-2003  (revised)
DT   12-DEC-1990  (first entry)
XX
DE   Sequence #21 recognised by probe for 16S RNA gene of mycoplasma.
XX
KW   Mollicutes.
XX
OS   Mycoplasma.
XX
PN   EP250662-A.
XX
PD   07-JAN-1988.
XX
PF   25-JUN-1986;   86EP-00304919.
XX
PR   25-JUN-1986;   86EP-00304919.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Gobel U,  Stanbridge EJ;
XX
DR   WPI; 1988-000726/01.
XX
PT   Detection of prokaryotic organisms - esp. mycoplasma by hybridisation
PT   with an oligo:nucleotide probe complementary to nucleotide sequence in
PT   the prokaryote.
XX
PS   Claim 16; Page 6; 9pp; English.
XX
CC   A probe which is complementary to this sequence can be used to detect
CC   prokaryotes. See also AAN82143-71. (Updated on 25-MAR-2003 to correct PA
CC   field.)
XX
SQ   Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 2.5;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db         19 TGCGGGACTTAACCCAACA 1


RESULT 8
AAV45647/c
ID   AAV45647 standard; DNA; 23 BP.
XX
AC   AAV45647;
XX
DT   04-MAR-1999  (first entry)
XX
DE   Probe for prokaryotic 16S RNA gene.
XX
KW   Probe; 16S RNA gene; mycoplasma; detection; prokaryote; diagnosis;
KW   bacteraemia; septicaemia; ss.
XX
OS   Synthetic.
XX
PN   US5851767-A.
XX
PD   22-DEC-1998.
XX
PF   06-JUN-1995;   95US-00469600.
XX
PR   04-MAR-1985;   85US-00707725.
PR   06-MAY-1988;   88US-00191852.
PR   27-NOV-1991;   91US-00799856.
PR   19-FEB-1993;   93US-00020874.
PR   14-OCT-1993;   93US-00136723.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Stanbridge EJ,  Gobel U;
```

XX
DR WPI; 1999-094418/08.
XX
PT Detection of mycoplasma-specific or prokaryote-specific nucleic acids -
PT using mycoplasma-specific or prokaryote-specific probes.
XX
PS Claim 3; Col 8; 11pp; English.
XX
CC This sequence represents a probe based on prokaryotic 16S RNA genes that
CC can be used in the method of the invention. The method is for detecting
CC the presence of prokaryotic specific nucleic acids, and comprises: (a)
CC contacting a medium, which may contain a nucleic acid or nucleic acid
CC fragment from the prokaryote having a particular nucleotide sequence,
CC with an oligonucleotide comprising a nucleotide sequence complementary to
CC the particular nucleotide sequence, whereby the oligonucleotide
CC hybridises with any nucleic acid or nucleic acid fragment from the
CC prokaryote which may be present in the medium; and (b) detecting the
CC presence of any nucleic acid or nucleic acid fragment hybridised with the
CC oligonucleotide. The invention also relates to a method for determining
CC the presence of a mycoplasma. The detection process is useful for
CC contaminated cell cultures or other biological environments. The probes
CC can be used in the diagnosis of bacteraemia or septicaemia in mammals.
CC The process provides a rapid, simple, effective, sensitive and specific
CC mycoplasma detection system. The probes can be made specific for
CC individual mycoplasma, acholeplasma, ureaplasma, spiroplasma, and
CC eubacterial species
XX
SQ Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19
||||||||||||||||||||
Db 19 TGCGGGACTTAACCCAACA 1

RESULT 9
AAV62776/c
ID AAV62776 standard; RNA; 23 BP.
XX
AC AAV62776;
XX
DT 04-MAR-1999 (first entry)
XX
DE Probe for prokaryotic 16S RNA gene.
XX
KW Probe; 16S RNA gene; mycoplasma; detection; prokaryote; diagnosis;
KW bacteraemia; septicaemia; ss.
XX
OS Synthetic.
XX
PN US5851767-A.
XX
PD 22-DEC-1998.
XX
PF 06-JUN-1995; 95US-00469600.
XX
PR 04-MAR-1985; 85US-00707725.
PR 06-MAY-1988; 88US-00191852.
PR 27-NOV-1991; 91US-00799856.
PR 19-FEB-1993; 93US-00020874.
PR 14-OCT-1993; 93US-00136723.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Stanbridge EJ, Gobel U;
XX
DR WPI; 1999-094418/08.
XX
PT Detection of mycoplasma-specific or prokaryote-specific nucleic acids -
PT using mycoplasma-specific or prokaryote-specific probes.
XX
PS Claim 19; Col 11; 11pp; English.
XX

```
CC   This sequence represents a probe based on prokaryotic 16S RNA genes that
CC   can be used in the method of the invention. The method is for detecting
CC   the presence of prokaryotic specific nucleic acids, and comprises: (a)
CC   contacting a medium, which may contain a nucleic acid or nucleic acid
CC   fragment from the prokaryote having a particular nucleotide sequence,
CC   with an oligonucleotide comprising a nucleotide sequence complementary to
CC   the particular nucleotide sequence, whereby the oligonucleotide
CC   hybridises with any nucleic acid or nucleic acid fragment from the
CC   prokaryote which may be present in the medium; and (b) detecting the
CC   presence of any nucleic acid or nucleic acid fragment hybridised with the
CC   oligonucleotide. The invention also relates to a method for determining
CC   the presence of a mycoplasma. The detection process is useful for
CC   contaminated cell cultures or other biological environments. The probes
CC   can be used in the diagnosis of bacteraemia or septicaemia in mammals.
CC   The process provides a rapid, simple, effective, sensitive and specific
CC   mycoplasma detection system. The probes can be made specific for
CC   individual mycoplasma, acholeplasma, ureaplasma, spiroplasma, and
CC   eubacterial species
XX
SQ   Sequence 23 BP; 5 A; 5 C; 7 G; 0 T; 6 U; 0 Other;

  Query Match             100.0%;  Score 19;  DB 2;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.5;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||
Db         19 TGCGGGACTTAACCCAACA 1


RESULT 10
AAZ44009/c
ID   AAZ44009 standard; DNA; 23 BP.
XX
AC   AAZ44009;
XX
DT   17-MAR-2000  (first entry)
XX
DE   Enterobacteriaceae detecting probe #2.
XX
KW   Detection; microorganism; primer; probe; cosmetic; food; ss.
XX
OS   Bacteria.
XX
PN   WO9958713-A2.
XX
PD   18-NOV-1999.
XX
PF   10-MAY-1999;   99WO-DE001471.
XX
PR   12-MAY-1998;   98DE-01022108.
XX
PA   (BIOI-) BIOINSIDE GMBH.
XX
PI   Gerbling K,  Lauter F,  Grohmann L;
XX
DR   WPI; 2000-072341/06.
XX
PT   A test kit for detecting microbially soiled, non sterile products,
PT   especially pharmaceuticals and cosmetics.
XX
PS   Example 26; Page 77; 77pp; German.
XX
CC   This invention describes a novel test kit to detect microbially soiled,
CC   non-sterile products, in particular after GMP-rich lines, also in
CC   cosmetics and food. The method involves the use of DNA fragment having a
CC   forward primer, probe, a reverse primer and if necessary a spacer
CC   oligonucleotide. The test kit and method are useful for economic
CC   detection of germs in pharmaceutical and cosmetic products. In particular
CC   the method is useful for detecting E. coli, P. aeruginosa, S. aureus and
CC   Salmonella
XX
SQ   Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 19;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.5;
```

```
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2


RESULT 11
AAH44156/c
ID   AAH44156 standard; DNA; 23 BP.
XX
AC   AAH44156;
XX
DT   14-SEP-2001  (first entry)
XX
DE   Escherichia coli 16S RNA gene oligonucleotide #10.
XX
KW   Mycoplasma; 16S RNA gene; infection; biological probe; detection;
KW   ribosomal RNA gene; prokaryote; ss.
XX
OS   Escherichia coli.
XX
PN   US6245509-B1.
XX
PD   12-JUN-2001.
XX
PF   14-SEP-1998;   98US-00152375.
XX
PR   04-MAR-1985;   85US-00707725.
PR   06-MAY-1988;   88US-00191852.
PR   27-NOV-1991;   91US-00799856.
PR   19-FEB-1993;   93US-00020874.
PR   14-OCT-1993;   93US-00136723.
PR   06-JUN-1995;   95US-00469600.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Stanbridge EJ,  Gobel UB;
XX
DR   WPI; 2001-416908/44.
XX
PT   Generating oligonucleotide probes, which are useful in DNA hybridization
PT   techniques for detecting mycoplasmas or prokaryotes in general.
XX
PS   Disclosure; Col 2; 6pp; English.
XX
CC   The present invention describes a method for obtaining oligonucleotide
CC   probes, comprising synthesising and isolating an oligonucleotide
CC   comprising a sequence identical to a sequence identified as hybridisable
CC   under predetermined conditions to a nucleotide sequence from one or more
CC   target organisms. The oligonucleotide probes are hybridisable to a
CC   nucleotide sequence contained by or specific to one or more target
CC   organisms but not to one or more selected non-target organisms in a
CC   sample. The target and non-target organisms do not have a cellular
CC   nucleus or are no higher phylogenetically than prokaryotes. The method
CC   comprises: (a) obtaining particular nucleotide sequence information of
CC   one or more of the target organisms; (b) obtaining particular nucleotide
CC   sequence information of one or more of the selected non-target organisms;
CC   (c) comparing the target and non-target sequence information and
CC   identifying from it at least one oligonucleotide sequence that is
CC   hybridisable under the predetermined conditions to a nucleotide sequence
CC   from the target organisms, but not to a nucleotide sequence of non-target
CC   organisms; and (d) synthesising and isolating an oligonucleotide
CC   comprising a sequence identical to the identified sequence. The method
CC   can be used for generating oligonucleotide probes for detecting
CC   mycoplasmas or prokaryotes in general. The present sequence represents an
CC   Escherichia coli 16S RNA gene oligonucleotide which is given in the
CC   exemplification of the present invention
XX
SQ   Sequence 23 BP; 5 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 19;  DB 4;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.5;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
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                  ||||||||||||||||||||
Db          19 TGCGGGACTTAACCCAACA 1
```

RESULT 12
ABK90486
ID   ABK90486 standard; DNA; 25 BP.
XX
AC   ABK90486;
XX
DT   05-NOV-2002 (first entry)
XX
DE   Synthetic polynucleotide probe #2.
XX
KW   Polycationic polymer; nucleic acid hybridisation; probe; ss;
KW   disease-associated gene; polymorphism.
XX
OS   Synthetic.
XX
PN   WO200248404-A2.
XX
PD   20-JUN-2002.
XX
PF   07-DEC-2001; 2001WO-US048592.
XX
PR   14-DEC-2000; 2000US-0255535P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Becker MM;
XX
DR   WPI; 2002-608283/65.
XX
PT   Forming duplexes from probe and target nucleic acid for diagnosing
PT   presence or absence of virus or organism in a sample, by conducting
PT   hybridization between the two in the presence of a synthetic polycationic
PT   polymer.
XX
PS   Example 2; Page 49; 63pp; English.
XX
CC   The invention relates to forming a duplex from a polynucleotide probe and
CC   a target nucleic acid comprising providing the probe to a test sample
CC   under conditions permitting the probe to preferentially hybridise to the
CC   target nucleic acid in the sample and providing a synthetic polycationic
CC   polymer to the sample which increases the association rate of the probe
CC   and the target nucleic acid. The method is useful for forming a duplex
CC   from a probe and a target nucleic acid comprising RNA (mRNA or rRNA). The
CC   probe preferentially hybridises to a target nucleic acid sequence
CC   contained in the target nucleic acid under the conditions, which is
CC   useful for diagnosing the presence or absence of a virus or organism or
CC   members of a group of viruses or organisms in the sample. The method is
CC   also useful for detecting the presence of a disease-associated gene,
CC   determining the state of a disease, measuring levels of gene expression
CC   and detecting mutations or polymorphisms in a test sample. This sequence
CC   represents a probe used in the method of the invention
XX
SQ   Sequence 25 BP; 6 A; 7 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match   100.0%; Score 19; DB 6; Length 25;
  Best Local Similarity   100.0%; Pred. No. 2.5;
  Matches   19; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy          1 TGCGGGACTTAACCCAACA 19
              ||||||||||||||||||||
Db          6 TGCGGGACTTAACCCAACA 24
```

RESULT 13
ADP47355/c
ID   ADP47355 standard; DNA; 25 BP.
XX
AC   ADP47355;
XX
DT   09-SEP-2004 (first entry)
XX
DE   Intelligent PCR primer for the identification of bacteria SeqID 10.

XX
KW PCR; ss; primer; pharmacogenetic analysis; medical diagnosis; cancer;
KW blood typing; virus stereotyping; pathogen; mass spectroscopy;
KW etiologic agent.
XX
OS Synthetic.
XX
PN WO2004052175-A2.
XX
PD 24-JUN-2004.
XX
PF 05-DEC-2003; 2003WO-US038830.
XX
PR 06-DEC-2002; 2002US-0431319P.
PR 18-DEC-2002; 2002US-00323233.
PR 18-DEC-2002; 2002US-00325526.
PR 18-DEC-2002; 2002US-00325527.
PR 18-DEC-2002; 2002US-00326051.
PR 29-JAN-2003; 2003US-0443443P.
PR 30-JAN-2003; 2003US-0443788P.
PR 14-FEB-2003; 2003US-0447529P.
PR 11-SEP-2003; 2003US-00660122.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey RH, Hofstadler SA, Sampath R, Mcneil J;
PI Crooke ST;
XX
DR WPI; 2004-468672/44.
XX
PT Identifying a pathogen in a biological sample, useful in medical
PT diagnosis, comprises amplifying a nucleic acid from the sample with a
PT pair of intelligent primers, and determining the molecular mass of the
PT amplification product.
XX
PS Example 15; SEQ ID NO 10; 228pp; English.
XX
CC This invention relates to a novel method for the rapid identification of
CC pathogens occurring in environmental samples or biological samples
CC derived from humans and animals. Specifically, it refers to using
CC intelligent primers to obtain an amplification product in order that the
CC molecular mass of the amplicon can be determined by mass spectroscopy,
CC which in turn identifies the pathogen found in the sample. The present
CC invention describes the rapid detection and identification of an
CC etiologic agent that does not required nucleic acid sequencing, and
CC instead relies on the use of intelligent primers to target ribosomal RNA
CC or housekeeping genes. Accordingly, this method can be used to identify a
CC pathogen or infectious agent in a biological sample, which is useful in
CC pharmacogenetic analysis and medical diagnosis (including cancer
CC diagnosis based on mutations and polymorphisms), or for detecting single
CC nucleotide polymorphisms in blood typing or stereotyping of viruses. This
CC oligonucleotide sequence is an intelligent PCR primer used to identify
CC different bacterial strains, given in an exemplification of the
CC invention.
XX
SQ Sequence 25 BP; 6 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19
||||||||||||||||||
Db 20 TGCGGGACTTAACCCAACA 2

RESULT 14
ADQ59713/c
ID ADQ59713 standard; DNA; 25 BP.
XX
AC ADQ59713;
XX
DT 07-OCT-2004 (first entry)
XX
DE Intelligent PCR primer 16S_EC_1082_1197 forward SEQ ID NO:10.
XX

KW ss; etiologic agent; disease; intelligent primer;
KW pathogen identification; PCR; primer.
XX
OS Synthetic.
XX
PN WO2004060278-A2.
XX
PD 22-JUL-2004.
XX
PF 05-DEC-2003; 2003WO-US038761.
XX
PR 06-DEC-2002; 2002US-0431319P.
PR 18-DEC-2002; 2002US-00323233.
PR 18-DEC-2002; 2002US-00325526.
PR 18-DEC-2002; 2002US-00325527.
PR 18-DEC-2002; 2002US-00326051.
PR 29-JAN-2003; 2003US-0443443P.
PR 30-JAN-2003; 2003US-0443788P.
PR 14-FEB-2003; 2003US-0447529P.
PR 11-SEP-2003; 2003US-0501926P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey RH, Sampath R, Hofstadler SA, Mcneil J;
PI Crooke ST, Blyn LB, Ranken R, Hall TA;
XX
DR WPI; 2004-534302/51.
XX
PT Identifying pathogens in humans or animals comprises amplifying a nucleic
PT acid molecule from the individual with intelligent primers to obtain
PT amplification products, and determining molecular masses of the
PT amplification products.
XX
PS Claim 40; SEQ ID NO 10; 184pp; English.
XX
CC The invention relates to a novel method for identifying etiologic agents
CC of disease in an individual comprising amplifying a nucleic acid from a
CC biological sample of the individual with intelligent primers to obtain
CC amplification products corresponding to the etiologic agents, and
CC determining the molecular masses of the amplification products. The
CC composition and methods of the invention are useful for identifying
CC pathogens in biological samples from humans and animals, resolving
CC etiologic agents present in samples obtained from humans and animals,
CC determining detailed genetic information about such pathogens or
CC etiologic agents, and for rapidly detecting and identifying bioagents
CC from environmental, clinical or other samples. The present sequence
CC represents an intelligent PCR primer of the invention.
XX
SQ Sequence 25 BP; 6 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGGGACTTAACCCAACA 19
||||||||||||||||||
Db 20 TGCGGGACTTAACCCAACA 2

RESULT 15
AED28542/c
ID AED28542 standard; DNA; 25 BP.
XX
AC AED28542;
XX
DT 15-DEC-2005 (first entry)
XX
DE Primer for PCR detection of 16S ribosomal RNA, SEQ ID NO:3.
XX
KW Microorganism detection; biological warfare; DNA identification;
KW DNA amplification; ss; primer; PCR; 16S ribosomal RNA.
XX
OS Escherichia coli.
XX
PN WO2005098047-A2.
XX

PD 20-OCT-2005.
XX
PF 18-FEB-2005; 2005WO-US005356.
XX
PR 18-FEB-2004; 2004US-0545425P.
PR 05-APR-2004; 2004US-0559754P.
PR 03-DEC-2004; 2004US-0632862P.
PR 22-DEC-2004; 2004US-0639068P.
PR 28-JAN-2005; 2005US-0648188P.
XX
PA (ISIS-) ISIS PHARM INC.
PA (SCIT-) SCI APPL INT CORP.
XX
PI Sampath R, Hall TA, Ecker DJ, Eschoo MW, Massire C, Larson BM;
PI Leighton T;
XX
DR WPI; 2005-703571/72.
XX
PT New oligonucleotide primer having a non-template tag, useful in preparing
PT a composition for determining the presence or absence of a bacterium of a
PT particular class, genus, species, or sub-species in a sample.
XX
PS Example 1; SEQ ID NO 3; 260pp; English.
XX
CC The new invention relates to genetic identification of bacteria.
CC Specifically claimed is a new oligonucleotide primer which has at least
CC one non-template tag. The primers are designed to produce bacterial
CC bioagent identifying amplicons of DNA encoding genes essential to life,
CC such as 16S, 23S rRNA, DNA-directed RNA polymerase subunits (rpoB and
CC rpoC), valyl-tRNA synthetase (valS), elongation factor EF-Tu (TufB),
CC ribosomal protein L2 (rplB), protein chain initiation factor (infB), and
CC spore protein (sspE). Also given is a composition comprising 1, 2 or more
CC of the oligonucleotide primers; a kit comprising the composition; a
CC method for identifying an unknown bacterium; a method of determining the
CC presence or absence of a bacterium of a particular class, genus, species,
CC or sub-species in a sample; and a method for determining the quantity of
CC an unknown bacterium in a sample. Either or both of the oligonucleotide
CC primers comprises at least one modified nucleobase, a non-templated T
CC residue on the 5'-end, at least one non-template tag, molecular mass
CC modifying tag or modified nucleobase. The oligonucleotide primers are
CC useful in preparing a composition for identifying an unknown bacterium,
CC determining the presence or absence of a bacterium of a particular class,
CC genus, species, or sub-species in a sample or determining the quantity of
CC an unknown bacterium in a sample. The present sequence is a primer from a
CC collection of primers used to identify bacteria using the described
CC methods. This primer detects a region of the gene encoding 16S ribosomal
CC RNA in an E.coli reference sequence.
XX
SQ Sequence 25 BP; 6 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db         20 TGCGGGACTTAACCCAACA 2
```

RESULT 16
AAN80834
ID AAN80834 standard; DNA; 26 BP.
XX
AC AAN80834;
XX
DT 25-MAR-2003 (revised)
DT 30-NOV-1990 (first entry)
XX
DE Probe no.3 for 16S rRNA of a broad phylogenetic range of bacteria.
XX
KW Bacteria; probe; 16S ribosomal RNA; ss.
XX
OS Synthetic.
XX
PN WO8803957-A.
XX

```
PD   02-JUN-1988.
XX
PF   24-NOV-1987;   87WO-US003009.
XX
PR   24-NOV-1986;   86US-00934244.
PR   07-AUG-1987;   87US-00083542.
XX
PA   (GENP-) GEN-PROBE INC.
PA   (HOGA/) HOGAN J J.
XX
DR   WPI; 1988-161626/23.
XX
PT   Probes for non-viral organisms - comprising an oligo:nucleotide
PT   complementary to a unique variable region r RNA sequence.
XX
PS   Claim 221; Page 161; 211pp; English.
XX
CC   The probe is designed to hybridise with 16S rRNA from a broad range of
CC   bacteria commonlyt found in urine but not to yeast or human rRNA. It
CC   corresponds to bases 1080-1110 of the E. coli 16S RNA and has a Tm of 67
CC   deg.C. See also AAN80785-N80851. (Updated on 25-MAR-2003 to correct PA
CC   field.)
XX
SQ   Sequence 26 BP; 6 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 19;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.5;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 17
AAN97224
ID   AAN97224 standard; DNA; 26 BP.
XX
AC   AAN97224;
XX
DT   06-JUL-1993  (first entry)
XX
DE   Probe contg. 5'-amine linker-arm.
XX
KW   Deoxyoligonucleotide; probe; amine; label; acridinium ester; AE;
KW   hybridisation assay; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /note= "comprises NH2-(CH2)6 as 5'-amine linker-arm"
XX
PN   WO8902476-A.
XX
PD   23-MAR-1989.
XX
PF   21-SEP-1988;   88WO-US003195.
XX
PR   21-SEP-1987;   87US-00099392.
XX
PA   (MLTE-) ML TECHN VENTURES.
XX
PI   Arnold L,  Nelson NC;
XX
DR   WPI; 1989-100016/13.
XX
PT   Homogeneous binding assay using degradable label esp. acridinium ester -
PT   with different stabilities in bound and unbound forms, esp. useful in
PT   hybridisation detection of specific polynucleotide.
XX
PS   Example 1(i); Page 20; 64pp; English.
XX
CC   Deoxyoligonucleotide probes were synthesised to contain an amine linker-
CC   arm (i.e., one which terminates in a primary amine for labelling with
```

```
CC   acridinium ester) located either at the 5'-terminus, at a specific
CC   preselected location along the polyphosphate chain, in the internal
CC   portion of the probe or attached to one of the nucleotide bases.
CC   Chemiluminescent acridinium ester labelled probes are used in homogeneous
CC   hybridisation assay format for sensitively detecting the presence of
CC   complementary target polynucleotide sequences
XX
SQ   Sequence 26 BP; 6 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 19;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.5;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 18
AAQ55675
ID   AAQ55675 standard; DNA; 26 BP.
XX
AC   AAQ55675;
XX
DT   25-MAR-2003  (revised)
DT   09-AUG-1994  (first entry)
XX
DE   Amine linker containing probe #1.
XX
KW   Probe; amine; linker arm; N-acridinium; ester; label; homogeneous;
KW   hybridisation assay; detection; linear dilution series; Chlamydia; rRNA;
KW   ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /label= NH2-(CH2)6-G
FT                   /note= "Amine linker arm"
XX
PN   US5283174-A.
XX
PD   01-FEB-1994.
XX
PF   08-NOV-1990;   90US-00613603.
XX
PR   21-SEP-1987;   87US-00099392.
PR   12-DEC-1988;   88US-00294700.
PR   23-MAY-1990;   90US-00528920.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Nelson NC,  Arnold LJ;
XX
DR   WPI; 1994-048084/06.
XX
PT   Homogeneous nucleic acid hybridisation assay - using probe labelled with
PT   acridinium ester for detection of linear dilution series.
XX
PS   Example 1; Col 12; 20pp; English.
XX
CC   This sequence represents a probe which contains an amine linker arm which
CC   may bear an N-acridinium ester label. Probes such as this may be used in
CC   an homogeneous hybridisation assay for determining the presence or amount
CC   of a target nucleic acid in a sample. This method comprises contacting
CC   the sample with a probe such as this, such that the acrinidium ester
CC   label may be degraded by a chemical, eg. acid, base or oxidising agent,
CC   while duplex-linked N-acrinidium ester remains undegraded. The
CC   hybridisation mixture is treated with the chemical and the amount of
CC   undegraded N-acrinidium ester is measured without physically separating
CC   any unhybridised probe. The method is capable of detecting linear
CC   dilution series, eg. Chlamydia rRNA with a detection limit of 0.1-1 ng.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 26 BP; 6 A; 8 C; 6 G; 6 T; 0 U; 0 Other;
```

```
  Query Match             100.0%;  Score 19;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.5;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25


RESULT 19
AAT73684
ID   AAT73684 standard; RNA; 26 BP.
XX
AC   AAT73684;
XX
DT   05-SEP-1997  (first entry)
XX
DE   RNA acridinium ester-labelled probe for adduct protection assay.
XX
KW   probe; assay; analyte; adduct protection; detection; acridinium ester;
KW   nucleic acid hybridisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    complement(1. .26)
FT                   /*tag=  b
FT                   /note= "used as target sequence - no label"
FT   modified_base   16
FT                   /*tag=  a
FT                   /note= "Acridinium ester labelled uracil"
XX
PN   EP747706-A1.
XX
PD   11-DEC-1996.
XX
PF   03-JUN-1996;   96EP-00108880.
XX
PR   07-JUN-1995;   95US-00478221.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Becker M,  Nelson NC;
XX
DR   WPI; 1997-023324/03.
XX
PT   Specific binding assay using signal-altering reagent - that
PT   preferentially alters signal of unbound probe.
XX
PS   Example 5; Page 16; 37pp; English.
XX
CC   Assaying for the presence of an analyte in a sample comprises using an
CC   adduct protection assay involving the use of a labelled binding partner
CC   and a signal altering ligand. The signal altering ligand can alter the
CC   signal from the label to a greater extent when the labelled binding
CC   partner is unbound than when it is bound to the analyte. The presence or
CC   amount of analyte can be determined by detecting the signal produced from
CC   unaltered label. The process is used especially for detecting nucleic
CC   acid (esp. RNA) sequences by homogeneous hybridisation assay. The assay
CC   is versatile, e.g. signal alteration can be effected under a wide range
CC   of conditions (e.g. pH, temperature and ionic strength) and both signal
CC   alteration and signal triggering can be effected at constant temperature
CC   to achieve high sensitivity. The relationship between adduct formation
CC   rates and the type of nucleic acid (RNA or DNA) present in the probe or
CC   target has been examined. It was found that adduct formation rates depend
CC   upon whether a probe and/or target is DNA or RNA and these rates do not
CC   directly correlate with the corresponding hydrolysis rates of labels
CC   identically associated with these molecules. The present sequence is an
CC   RNA AE-labelled probe
XX
SQ   Sequence 26 BP; 6 A; 8 C; 6 G; 0 T; 6 U; 0 Other;

  Query Match             100.0%;  Score 19;  DB 2;  Length 26;
  Best Local Similarity   84.2%;  Pred. No. 2.5;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 TGCGGGACTTAACCCAACA 19
              :|||||||::|||||||||
Db          7 UGCGGGACUUAACCCAACA 25


RESULT 20
AAT73680
ID   AAT73680 standard; DNA; 26 BP.
XX
AC   AAT73680;
XX
DT   05-SEP-1997  (first entry)
XX
DE   Acridinium ester labelled probe 3 for adduct protection assay.
XX
KW   probe; assay; analyte; adduct protection; detection; acridinium ester;
KW   nucleic acid hybridisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    complement(1. .26)
FT                   /*tag=  b
FT                   /note= "used as target sequence - no label"
FT   modified_base   16
FT                   /*tag=  a
FT                   /note= "Acridinium ester labelled thymine"
XX
PN   EP747706-A1.
XX
PD   11-DEC-1996.
XX
PF   03-JUN-1996;   96EP-00108880.
XX
PR   07-JUN-1995;   95US-00478221.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Becker M,  Nelson NC;
XX
DR   WPI; 1997-023324/03.
XX
PT   Specific binding assay using signal-altering reagent - that
PT   preferentially alters signal of unbound probe.
XX
PS   Example 3; Page 13; 37pp; English.
XX
CC   Assaying for the presence of an analyte in a sample comprises using an
CC   adduct protection assay involving the use of a labelled binding partner
CC   and a signal altering ligand. The signal altering ligand can alter the
CC   signal from the label to a greater extent when the labelled binding
CC   partner is unbound than when it is bound to the analyte. The presence or
CC   amount of analyte can be determined by detecting the signal produced from
CC   unaltered label. The process is used especially for detecting nucleic
CC   acid (esp. RNA) sequences by homogeneous hybridisation assay. The assay
CC   is versatile, e.g. signal alteration can be effected under a wide range
CC   of conditions (e.g. pH, temperature and ionic strength) and both signal
CC   alteration and signal triggering can be effected at constant temperature
CC   to achieve high sensitivity. The effect different acridinium ester (AE)
CC   derivative structures have on adduct formation rates was measured using
CC   the present sequence as the AE-labelled probe and its complement as the
CC   target. AE having unsubstituted acridinium rings form adducts with sodium
CC   sulphite and metabisulphite at about the same rate. In contrast 1-methyl-
CC   AE and 2,7-di-methyl-AE formed adducts more than ten times slower than
CC   the unsubstituted AE derivatives
XX
SQ   Sequence 26 BP; 6 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 19;  DB 2;  Length 26;
  Best Local Similarity  100.0%;  Pred. No. 2.5;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGCGGGACTTAACCCAACA 19
              |||||||||||||||||||
Db          7 TGCGGGACTTAACCCAACA 25
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Search completed: July 26, 2006, 15:58:55
Job time : 214.707 secs

SCORE 1.3 BuildDate: 12/06/2005

BN): X87272
GenBank VERSION (VER): X87272.1 GI:1165003
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SEQUENCE LENGTH (SQL): 1484
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Bacteria
DATE (DATE): 22 Jan 1996
DEFINITION (DEF): B.japonicum 16S rRNA gene.
SOURCE: Bradyrhizobium japonicum.
ORGANISM (ORGN): Bradyrhizobium japonicum
Bacteria; Proteobacteria; alpha subdivision;
Rhizobiaceae group; Bradyrhizobium group;
Bradyrhizobium
NUCLEIC ACID COUNT (NA): 361 a 356 c 465 g 298 t 4 others
REFERENCE: 1 (bases 1 to 1484)
AUTHOR (AU): Ludwig,W.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (18-MAY-1995) W. Ludwig, Lehrstuhl fuer
Mikrobiologie, Technische Universitaet Muenchen,
Muenchen, FRG
REFERENCE: 2 (bases 1 to 1484)
AUTHOR (AU): Ludwig,W.; Rossello-Mora,R.; Aznar,R.; Klugbauer,S.;
Spring,S.; Reetz,K.; Beimfohr,C.; Brockmann,E.;
Kirchhof,G.; Dorn,S.; Bachleitner,M.; Klugbauer,N.;
Springer,N.; Lane,D.; Nietupsky,R.; Weizenegger,M.;
Schleifer,K.H.
TITLE (TI): Comparative sequence analysis of 23S rRNA from
proteobacteria
JOURNAL (SO): Syst. Appl. Microbiol., 18, 164-188 (1995)
OTHER SOURCE (OS): CA 124:195266

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..1484	/organism="Bradyrhizobium japonicum" /strain="DSM 30131 T" /db-xref="taxon:375"
rRNA	1..1484	/gene="16S rRNA" /product="16S ribosomal RNA"
gene	1..1484	/gene="16S rRNA"

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   121 tcggaacaac acagggaaac ttgtgctaat accggataag cccttacggg gaaagattta
   181 tcgccgaaag atcggcccgc gtctgattag ctagttggta gggtaacggc ctaccaaggc
   241 gacgatcagt agctggtctg agaggatgat cagccacatt gggactgaga cacggcccaa
   301 actcctacgg gaggcagcag tggggaatat tggacaatgg gggcaaccct gatccagcca
   361 tgccgcgtga gtgatgaagg ccctagggtt gtaaagctct tttgtgcggg aagataatga
   421 cggtaccgca agaataagcc ccggctaact tcgtgccagc agccgcggta atacgaaggg
   481 ggctagcgtt gctcggaatc actgggcgta aagggtgcgt aggcgggtct ttaagtcagg
   541 ggtgaaatcc tggagctcaa ctccagaact gcctttgata ctgaagatct tgagttcggg
   601 agaggtgagt ggaactgcga gtgtagaggt gaaattcgta gatattcgca agaacaccag
   661 tggcgaaggc ggctcactgg cccgatactg acgctgaggc acgaaagcgt ggggagcaaa
   721 caggattaga taccctggta gtccacgccg taaacgatga atgccagccg ttagtgggtt
   781 tactcactag tggcgcagct aacgctttaa gcattccgcc tggggagtac ggtcgcaaga
   841 ttaaaactca aaggaattga cgggggcccg cacaagcggt ggagcatgtg gtttaattcg
   901 acgcaacgcg cagaacctta ccagcccttg acatgtccag gaccggtcgc agagatgtga
   961 ccttctcttc ggagcctgga acacaggtgc tgcatggctg tcgtcagctc gtgtcgtgag
  1021 atgttgggtt aagtcccgca acgagcgcaa cccccgtcct tagttgctac catttagttg
  1081 agcactctaa ggagactgcc ggtgataagc cgcgaggaag gtggggatga cgtcaagtcc
  1141 tcatggccct tacgggctgg gctacacacg tgctacaatg gcggtgacaa tgggatgcta
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Bradyrhizobium japonicum gene for 16S rRNA, strain: IAM 12608.

SOURCE: Bradyrhizobium japonicum
ORGANISM (ORGN): Bradyrhizobium japonicum
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium
REFERENCE: 1 (bases 1 to 1441)
AUTHOR (AU): Yanagi,M.; Yamasato,K.
TITLE (TI): Phylogenetic analysis of the family Rhizobiaceae and related bacteria by sequencing of 16S rRNA gene using PCR and DNA sequencer
JOURNAL (SO): FEMS Microbiol. Lett., 107 (1), 115-120 (1993)
OTHER SOURCE (OS): CA 119:155937
REFERENCE: 2 (bases 1 to 1441)

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  1201 aggggcgacc cttcgcaaat ctcaaaaagc cgtctcagtt cggattgggc tctgcaactc
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  1321 ccgggccttg tacacaccgc ccgtcacacc atgggagttg gctttacctg aagacggtgc
  1381 gctaacctgc aaaggaggca gccggccacg gtagggtcag cgactggggt gaagtcgtaa
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L2 ANSWER 2 OF 2 GENBANK® COPYRIGHT 2006 on STN

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LOCUS (LOC):                BJ23SRRN     GenBank (R)
GenBank ACC. NO. (GBN):     X71840
GenBank VERSION (VER):      X71840.1  GI:468567
CAS REGISTRY NO. (RN):      154450-08-5
SEQUENCE LENGTH (SQL):      2882
MOLECULE TYPE (CI):         DNA; linear
DIVISION CODE (CI):         Bacteria
DATE (DATE):                28 Mar 1994
DEFINITION (DEF):           B.japonicum 16S rRNA gene.
SOURCE:                     Bradyrhizobium japonicum.
 ORGANISM (ORGN):           Bradyrhizobium japonicum
                            Bacteria; Proteobacteria; alpha subdivision;
                            Rhizobiaceae group; Bradyrhizobium group;
                            Bradyrhizobium
NUCLEIC ACID COUNT (NA): 751 a   656 c   887 g   588 t
REFERENCE:                  1  (bases 1 to 2882)
   AUTHOR (AU):             Springer,N.; Ludwig,W.; Hardarson,G.
   TITLE (TI):              A 23S rRNA targeted specific hybridization probe for
                            Bradyrhizobium japonicum
   JOURNAL (SO):            Syst. Appl. Microbiol., 16, 468-470 (1993)
   OTHER SOURCE (OS):       CA 120:262524
REFERENCE:                  2  (bases 1 to 2882)
   AUTHOR (AU):             Ludwig,W.
   TITLE (TI):              Direct Submission
   JOURNAL (SO):            Submitted (05-MAY-1993) W. Ludwig, Lehrst. f.
                            Mikrobiologie TU Muenchen, Arcisstr. 21, 8000 Muenchen
                            2, FRG

FEATURES (FEAT):
  Feature Key       Location                Qualifier
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source          1..2882                 /organism="Bradyrhizobium
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                                        /db-xref="taxon:375"
rRNA            1..2882                 /product="23S ribosomal RNA"

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1141 tgtggaaatc ccaaaacaac caggaggttg gcttagaagc agccatcctt taaagaaagc
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1261 acgagccgaa gcttagggtg tgatccgcaa gggtcacgcg gtagcggagc gttctgtaag
1321 cctgcgaagg gcgactcgtg agagcgcctg gaggtatcag aagtgcgaat gctggcatga
1381 gtaacgacaa acactgtgaa agacagtgtc gccgaaagtc caagggttcc tgcgtaaagt
1441 taatcttcgc agggttagcc ggtccctaag gcgaggccga aaggcgtagt cgatgggaat
1501 gcagtgaata ttctgcagcc agtggatggt gacgaatccc gtgtgttgtc cgaccttact
1561 ggattggttg ggcttcgaag gggttccagg aaatagcctc cacatcagac cgtacccgaa
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1801 gcaagatgac gtatagggtc tgacgcctgc ccggtgccgg aaggttaaga ggagaggtgc
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2101 aataggtggt aggctttgaa gccgtggcgc cagccatggt ggagccgaaa tgtgaaatac
2161 caccctaatg gttatggata tctaaccgcg tcccctcagc ggggaccggg acagcgcatg
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2581 gtgagacagt tcggtcccta tctgccgtgg gtgttggaat gttgagagga tttgccccta
2641 gtacgagagg accggggtga acgtacctct ggtggagctg ttgtcgcgcc agcggcagtg
2701 cagcatagct atgtacggac gggataaccg ctgaaagcat ctaagcggga aacccacctc
2761 aaaacgagca ttcccttgag aaccgtggaa gaccaccacg ttgataggcc gggtgtggaa
2821 gtgcagtaat gcatgcagct taccggtact aatcgttcga ttggcttgat tgctctcatt
2881 tt
```

=>

Use of real-time PCR and fluorimetry for rapid detection of rifampin and isoniazid resistance-associated mutations in Mycobacterium tuberculosis

AUTHOR: TORRES M. J.; CRIADO A.; PALOMARES J. C.; AZNAR J.

CORPORATE SOURCE: Unidad de Microbiologia Molecular, Departamento de Microbiologia, Universidad de Sevilla, 41080 Seville, Spain

SOURCE: Journal of clinical microbiology, (2000), 38(9), 3194-3199, 24 refs.
ISSN: 0095-1137 CODEN: JCMIDW

DOCUMENT TYPE: Journal

BIBLIOGRAPHIC LEVEL: Analytic

COUNTRY: United States

LANGUAGE: English

AVAILABILITY: INIST-17088, 354000091289690100

AN 2000-0532525 PASCAL

AB Very fast amplification of DNA in small volumes can be continuously monitored with a rapid cycler that incorporates fluorimetric detection. Primers were designed to amplify a 157-bp fragment of the rpoB gene spanning codons 526 and 531 and a 209-bp fragment of the katG gene spanning codon 315 of Mycobacterium tuberculosis. Most mutations associated with resistance to rifampin (RMP) and isoniazid (INH) in clinical isolates occur in these codons. Two pairs of hybridization probes were synthesized; one in each pair was 3' labeled with fluorescein and hybridized upstream of the codon with the mutation; the other two probes were 5' labeled with LightCycler-Red 640. Each pair of probes recognized adjacent sequences in the amplicon. After DNA amplification was finished by using a LightCycler, the temperature at which the Red 640 probe melted from the product was determined in a 3-min melt program. Twenty M. tuberculosis clinical isolates susceptible to streptomycin, INH, RMP, and ethambutol and 36 antibiotic-resistant clinical M. tuberculosis isolates (16 resistant to RMP, 16 to INH, and 4 to both antimicrobial agents) were amplified, and the presence of mutations was determined using single-strand conformation polymorphism analysis, the LiQor automated sequencer, and the LightCycler system. Concordant results were obtained in all cases. Within 30 min, the LightCycler method correctly genotyped all the strains without the need of any post-PCR sample manipulation. Overall, this pilot study demonstrated that real-time PCR coupled to fluorescence detection is the fastest available method for the detection of RMP and INH resistance-associated mutations in M. tuberculosis clinical isolates.

L5 ANSWER 23 OF 31 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2004:418561 SCISEARCH

THE GENUINE ARTICLE: 814GK

TITLE: Direct detection of rifampin- and isoniazid-resistant Mycobacterium tuberculosis in auramine-rhodamine-positive sputum specimens by real-time PCR

AUTHOR: Ruiz M; Torres M J (Reprint); Llanos A C; Arroyo A; Palomares J C; Aznar J

CORPORATE SOURCE: Fac Med, Dept Microbiol, Apdo 914, Seville 41080, Spain (Reprint); HH UU Virgen del Rocio, Microbiol Serv, Seville, Spain; Univ Sevilla, Unidad Microbiol Mol, Dept Microbiol, Seville, Spain

COUNTRY OF AUTHOR: Spain

SOURCE: JOURNAL OF CLINICAL MICROBIOLOGY, (APR 2004) Vol. 42, No. 4, pp. 1585-1589.
ISSN: 0095-1137.

PUBLISHER: AMER SOC MICROBIOLOGY, 1752 N ST NW, WASHINGTON, DC 20036-2904 USA.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 30
ENTRY DATE: Entered STN: 21 May 2004
Last Updated on STN: 21 May 2004
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Our objective was to evaluate the feasibility of a molecular assay based on a real-time PCR technique, carried out with a LightCycler instrument (Roche Biochemicals), to identify Mycobacterium tuberculosis bacilli and to detect rifampin and isoniazid resistance in DNA extracts from sputum samples. We studied three genes: rpoB, which is associated with rifampin resistance, and katG and inhA, which are associated with isoniazid resistance. A total of 205 sputum samples collected from 108 patients diagnosed with pulmonary tuberculosis with positive auramine-rhodamine-staining (AR) sputum samples, were tested. The sensitivities of the LightCycler PCR assay for the positive AR specimens was 97.5% (200 of 205) for rpoB? and inhA genes and 96.5% (198 of 205) for the katG gene. For the total number of patients tested, the sensitivity was 100% (108 of 108 patients) for rifampin, whereas the sensitivity was 98.1% (106 of 108 patients) for isoniazid. Full agreement was found with the Bactec MGIT 960 method and the genotype inferred from the LightCycler data for rifampin. The phenotypic method for isoniazid reported 13 resistant strains (greater than or equal to0.1 mug/ml). In seven (53.8%) strains there was a concordance between both methods, but we found that six (46.2%) strains reported as resistant by the phenotypic method were determined to be susceptible by real-time PCR. For the 75 strains reported as susceptible by the phenotypic method, the concordance with the LightCycler data was 100%. Our results demonstrate that rifampin-resistant M. tuberculosis could be detected in DNA extracted from auramine-rhodamine-positive sputum samples in a single-tube assay that took less than 3 h to perform for a collection of auramine-rhodamine-positive specimens obtained from patients with culture-documented pulmonary tuberculosis. Similarly, this occurs in half of the isoniazid-resistant M. tuberculosis DNA extracted from auramine-rhodamine-positive specimens.

FILE 'MEDLINE, AGRICOLA, ANTE, AQUALINE, BIOSIS, BIOTECHNO, CABA, CAPLUS, CBNB, CIN, CONFSCI, CROPB, CROPU, DISSABS, ENVIROENG, ESBIOBASE, FOMAD, FOREGE, FROSTI, FSTA, GENBANK, IFIPAT, INVESTEXT, LIFESCI, NAPRALERT, NTIS, PASCAL, PHIC, PHIN, PROMT, ...' ENTERED AT 15:53:46 ON 31 JUL 2006

L1 303119 S (BRADHYRHIZOBIUM OR JAPONICUM OR RHIZOBIUM)
L2 85 S L1 AND ((REAL-TIME PCR) OR (REAL TIME (3A) POLYMERASE CHAIN
L3 59 DUP REM L2 (26 DUPLICATES REMOVED)

=> d l3 ti 1-59

L3 ANSWER 1 OF 59 USPATFULL on STN
TI Receptors and membrane-associated proteins

L3 ANSWER 2 OF 59 USPATFULL on STN
TI Treatment of fibrosis using FXR ligands

L3 ANSWER 3 OF 59 USPATFULL on STN
TI Molecules for disease detection and treatment

L3 ANSWER 4 OF 59 USPATFULL on STN
TI Genus, group, species and/or strain specific 16S rDNA sequences

L3 ANSWER 5 OF 59 USPATFULL on STN
TI Nucleic acid and polypeptide sequences from Lawsonia intracellularis and methods of using

L3 ANSWER 6 OF 59 USPATFULL on STN
TI Identification of novel e2f target genes and use thereof

L3 ANSWER 7 OF 59 USPATFULL on STN
TI Genomic barcoding for organism identification

L3 ANSWER 8 OF 59 USPATFULL on STN
TI Proteome epitope tags and methods of use thereof in protein modification analysis

L3 ANSWER 9 OF 59 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
TI Transcriptome profiling of lung schistosomula, in vitro cultured schistosomula and adult Schistosoma japonicum;
lung schistosomula, in vitro cultured schistosomula and adult Schistosoma japonicum transcriptome expression profiling for transcriptomics

L3 ANSWER 10 OF 59 MEDLINE on STN DUPLICATE 1
TI Dynamics of CD4+CD25+ T cells in spleens and mesenteric lymph nodes of mice infected with Schistosoma japonicum.

L3 ANSWER 11 OF 59 Elsevier BIOBASE COPYRIGHT 2006 Elsevier Science B.V. on STN
TI The transformation of betA gene into the pollen plantlets of Populus simoniixP. nigra

L3 ANSWER 12 OF 59 MEDLINE on STN DUPLICATE 2
TI Design and validation of a partial-genome microarray for transcriptional profiling of the Bradyrhizobium japonicum symbiotic gene region.

L3 ANSWER 13 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 3
TI Isolation and mutagenesis of broad host range pBBR1-based plasmids having altered plasmid copy number

L3 ANSWER 14 OF 59 IFIPAT COPYRIGHT 2006 IFI on STN DUPLICATE 4
TI BROAD HOST RANGE PBBR1-BASED PLASMID MUTANT DERIVATIVES HAVING ALTERED

PLASMID COPY NUMBER

L3 ANSWER 15 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Identification of Rhizobium species clogging activated sludge separation membrane based on 16S rRNA gene sequence

L3 ANSWER 16 OF 59 USPATFULL on STN
TI Small molecule and peptide arrays and uses thereof

L3 ANSWER 17 OF 59 USPATFULL on STN
TI Gene products differentially expressed in cancerous cells and their methods of use II

L3 ANSWER 18 OF 59 USPATFULL on STN
TI Protein modification and maintenance molecules

L3 ANSWER 19 OF 59 USPATFULL on STN
TI Compositions and methods for treating diseases

L3 ANSWER 20 OF 59 USPATFULL on STN
TI Enzymes

L3 ANSWER 21 OF 59 USPATFULL on STN
TI Nucleic acid-associated proteins

L3 ANSWER 22 OF 59 USPATFULL on STN
TI Kinases and phosphatases

L3 ANSWER 23 OF 59 USPATFULL on STN
TI Protein

L3 ANSWER 24 OF 59 USPATFULL on STN
TI Secreted proteins

L3 ANSWER 25 OF 59 USPATFULL on STN
TI Enzymes

L3 ANSWER 26 OF 59 USPATFULL on STN
TI Compositions and methods for treating inflammatory disorders

L3 ANSWER 27 OF 59 USPATFULL on STN
TI Receptors and membrane-associated proteins

L3 ANSWER 28 OF 59 USPATFULL on STN
TI Protein modification and maintenance molecules

L3 ANSWER 29 OF 59 USPATFULL on STN
TI Therapeutic treatment methods 2

L3 ANSWER 30 OF 59 USPATFULL on STN
TI Manipulation of flavonoid biosynthesis in plants

L3 ANSWER 31 OF 59 USPATFULL on STN
TI Proteins associated with cell growth, differentiation, and death

L3 ANSWER 32 OF 59 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI Transcript enrichment of Nod factor-elicited early nodulin genes in purified root hair fractions of the model legume Medicago truncatula.

L3 ANSWER 33 OF 59 EMBASE COPYRIGHT (c) 2006 Elsevier B.V. All rights reserved on STN
TI Techniques for detecting genetically modified crops and products.

L3 ANSWER 34 OF 59 Elsevier BIOBASE COPYRIGHT 2006 Elsevier Science B.V. on STN
TI Expression levels of avrBs3-like genes affect recognition specificity in tomato Bs4- but not in pepper Bs3-mediated perception

L3 ANSWER 35 OF 59 MEDLINE on STN DUPLICATE 5
TI Symbiotic and saprophytic survival of three unmarked Rhizobium leguminosarum biovar trifolii strains introduced into the field.

L3 ANSWER 36 OF 59 EMBASE COPYRIGHT (c) 2006 Elsevier B.V. All rights reserved on STN
TI Directed evolution of copy number of a broad host range plasmid for metabolic engineering.

L3 ANSWER 37 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 6
TI Assays and devices for detecting microbial contamination in animal by-products

L3 ANSWER 38 OF 59 IFIPAT COPYRIGHT 2006 IFI on STN DUPLICATE 7
TI QUANTITATIVE ASSAY FOR THE SIMULTANEOUS DETECTION AND SPECIATION OF BACTERIAL INFECTIONS

L3 ANSWER 39 OF 59 IFIPAT COPYRIGHT 2006 IFI on STN
TI QUANTITATIVE ASSAY FOR THE SIMULTANEOUS DETECTION AND SPECIATION OF BACTERIAL INFECTIONS; ADAPTATION OF THE REAL-TIME PCR ASSAY ALLOWS FOR HIGHLY SENSITIVE DETECTION OF ANY EUBACTERIAL SPECIES WITH SIMULTANEOUS SPECIATION. THE ASSAY RELIES ON A 'MULTIPROBE' DESIGN IN WHICH A SINGLE SET OF HIGHLY CONSERVED SEQUENCES

L3 ANSWER 40 OF 59 USPATFULL on STN
TI Vesicle-associated proteins

L3 ANSWER 41 OF 59 USPATFULL on STN
TI Adiponectin receptor and gene encoding the same

L3 ANSWER 42 OF 59 USPATFULL on STN
TI Detecting microbial contamination in grain and related products

L3 ANSWER 43 OF 59 USPATFULL on STN
TI Compositions and methods for treating neurological disorders and diseases

L3 ANSWER 44 OF 59 USPATFULL on STN
TI Compositions and methods for treating diabetes

L3 ANSWER 45 OF 59 USPATFULL on STN
TI Methods for improving plant agronomical traits by altering the expression or activity of plant G-protein alpha and beta subunits

L3 ANSWER 46 OF 59 USPATFULL on STN
TI Cpn60 targets for quantification of microbial species

L3 ANSWER 47 OF 59 USPATFULL on STN
TI Detecting hormonally active compounds

L3 ANSWER 48 OF 59 USPATFULL on STN
TI Detection and quantification of aromatic oxygenase genes by real -time PCR

L3 ANSWER 49 OF 59 USPATFULL on STN
TI Therapeutic treatment methods

L3 ANSWER 50 OF 59 USPATFULL on STN
TI Method of selecting antimicrobial agent and method of using the same

L3 ANSWER 51 OF 59 USPATFULL on STN
TI Monitoring high-risk environments

L3 ANSWER 52 OF 59 MEDLINE on STN DUPLICATE 8
TI Highly up-regulated CXCR3 expression on eosinophils in mice infected with Schistosoma japonicum.

L3 ANSWER 53 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Expression of hemoglobin genes in actinorhizal plant (non-leguminous plant symbiosis with Frankia)

L3 ANSWER 54 OF 59 IFIPAT COPYRIGHT 2006 IFI on STN DUPLICATE 9
TI QUANTITATIVE ASSAY FOR THE SIMULTANEOUS DETECTION AND SPECIATION OF BACTERIAL INFECTIONS; ADAPTATION OF THE REAL-TIME PCR ASSAY ALLOWS FOR HIGHLY SENSITIVE DETECTION OF ANY EUBACTERIAL SPECIES WITH SIMULTANEOUS SPECIATION. THE ASSAY RELIES ON A 'MULTIPROBE' DESIGN IN WHICH A SINGLE SET OF HIGHLY CONSERVED SEQUENCES

L3 ANSWER 55 OF 59 USPATFULL on STN DUPLICATE 10
TI Histoplasma capsulatum catalase sequences and their use in the detection of Histoplasma capsulatum and Histoplasmosis

L3 ANSWER 56 OF 59 MEDLINE on STN
TI Pleiotropic effect of the insertion of the Agrobacterium rhizogenes rolD gene in tomato (Lycopersicon esculentum Mill.).

L3 ANSWER 57 OF 59 CAPLUS COPYRIGHT 2006 ACS on STN
TI Highly up-regulated CXCR3 expression on eosinophils in mice infected with Schistosoma japonicum

L3 ANSWER 58 OF 59 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
TI Detecting and determining species source of eubacterial DNA in a sample, comprises amplifying template DNA in the sample using a real-time polymerase chain reaction with the use of primers and at least two fluorogenic probes; bacterium DNA detection and polymerase chain reaction

L3 ANSWER 59 OF 59 USPATFULL on STN
TI Modulation of mitochondrial mass and function for the treatment of diseases and for target and drug discovery

=>

Proteomic analysis of soybean root hairs after infection by Bradyrhizobium japonicum

AUTHOR: Wan J R; Torres M; Ganapathy A; Thelen J; DaGue B B; Mooney B; Xu D; Stacey G (Reprint)

CORPORATE SOURCE: Univ Missouri, Natl Ctr Soybean Biotechnol, Dept Microbiol & Plant Pathol, Columbia, MO 65211 USA (Reprint); Maryville Coll, Dept Biol, Maryville, TN 37804 USA; Univ Missouri, Dept Comp Sci, Columbia, MO 65211 USA; Univ Missouri, Dept Biochem, Columbia, MO 65211 USA; Univ Missouri, Proteom Ctr, Columbia, MO 65211 USA staceyg@missouri.edu

COUNTRY OF AUTHOR: USA

SOURCE: MOLECULAR PLANT-MICROBE INTERACTIONS, (MAY 2005) Vol. 18, No. 5, pp. 458-467.
ISSN: 0894-0282.

PUBLISHER: AMER PHYTOPATHOLOGICAL SOC, 3340 PILOT KNOB ROAD, ST PAUL, MN 55121 USA.

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LANGUAGE: English

REFERENCE COUNT: 68

ENTRY DATE: Entered STN: 5 May 2005
Last Updated on STN: 5 May 2005

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Infection of soybean root hairs by Bradyrhizobium japonicum is the first of several complex events leading to nodulation. In the current proteomic study, soybean root hairs after inoculation with B. japonicum were separated from roots. Total proteins were analyzed by two-dimensional (2-D) polyacrylamide gel electrophoresis. In one experiment, 96 protein spots were analyzed by matrix-assisted laser desorption ionization time-of-flight (MALDI-TOF) mass spectrometry (MS) to compare protein profiles between uninoculated roots and root hairs. Another 37 spots, derived from inoculated root hairs over different timepoints, were also analyzed by tandem NIS (MS/MS). As expected, some proteins were differentially expressed in root hairs compared with roots (e.g., a chitinase and phosphoenolpyruvate carboxylase). Out of 37 spots analyzed by MS/MS, 27 candidate proteins were identified by database comparisons. These included several proteins known to respond to rhizobial inoculation (e.g., peroxidase and phenylalanine-ammonia lyase). However, novel proteins were also identified (e.g., phospholipase D and phosphoglucomutase). This research establishes an excellent system for the study of root-hair infection by rhizobia and, in a more general sense, the functional genomics of a single, plant cell type. The results obtained also indicate that proteomic studies with soybean, lacking a complete genome sequence, are practical.

=> end

PubMed ID: 11159974
TITLE: Identification of Rgg-regulated exoproteins of Streptococcus pyogenes.
AUTHOR: Chaussee M S; Watson R O; Smoot J C; Musser J M
CORPORATE SOURCE: Laboratory of Human Bacterial Pathogenesis, Rocky Mountain Laboratories, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Hamilton, Montana 59840, USA.
SOURCE: Infection and immunity, (2001 Feb) Vol. 69, No. 2, pp. 822-31.
Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 4 Apr 2001
Last Updated on STN: 4 Apr 2001
Entered Medline: 15 Mar 2001
AB Streptococcus pyogenes secretes many proteins that influence host-pathogen interactions. Despite their importance, relatively little is known about the regulation of these proteins. The rgg gene (also known as ropB) is required for the expression of streptococcal erythrogenic toxin B (SPE B), an extracellular cysteine protease that contributes to virulence. Proteomics was used to determine if rgg regulates the expression of additional exoproteins. Exponential- and stationary-phase culture supernatant proteins made by S. pyogenes NZ131 rgg and NZ131 speB were separated by two-dimensional electrophoresis. Differences were identified in supernatant proteins from both exponential- and stationary-phase cultures, although considerably more differences were detected among stationary-phase supernatant proteins. Forty-two proteins were identified by peptide fingerprinting with matrix-assisted laser desorption mass spectrometry. Mitogenic factor, DNA entry nuclease (open reading frame [ORF 226]), and ORF 953, which has no known function, were more abundant in the culture supernatants of the rgg mutant compared to the speB mutant. ClpB, lysozyme, and autolysin were detected in the culture supernatant of the speB mutant but not the rgg mutant. To determine if Rgg affected protein expression at the transcriptional level, real-time (TaqMan) reverse transcription (RT)-PCR was used to quantitate Rgg-regulated transcripts from NZ131 wild-type and speB and rgg mutant strains. The results obtained with RT-PCR correlated with the proteomic data. We conclude that Rgg regulates the transcription of several genes expressed primarily during the stationary phase of growth.

PubMed ID: 11159974
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AUTHOR: Chaussee M S; Watson R O; Smoot J C; Musser J M
CORPORATE SOURCE: Laboratory of Human Bacterial Pathogenesis, Rocky Mountain Laboratories, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Hamilton, Montana 59840, USA.
SOURCE: Infection and immunity, (2001 Feb) Vol. 69, No. 2, pp. 822-31.
Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 4 Apr 2001
Last Updated on STN: 4 Apr 2001
Entered Medline: 15 Mar 2001

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